

(TM)

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protein - protein database search, using Smith-Waterman algorithm

Wed Apr 19 21:55:40 2000; MasPar time 83.73 Seconds

Output not generated.

1 MASPRSSGQPPPPPPPP...TASPRHRHVPSPFRVMVSGL 941

able:	PAM	150
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225878 seqs, 69334122 residues

Listing first 45 summaries

1:sp. archaea 2:sp. bacteria 3:sp. fungi 4:sp. human
5:sp. invertebrate 6:sp. mammal 7:sp. mhc 8:sp. organelle
9:sp. phage 10:sp. plant 11:sp. rodent 12:sp. unclassified
13:sp. vertebrate 14:sp. virus

Mean 54.905; Variance 107.024; scale 0.513

11. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

Score	Query Match	Length	DB	ID	Description	Prod. No.
1905	100.0	94.1	4	075899	GABA-B RECEPTOR.	0.00e+00
1760	97.9	940	11	088871	GABA-B RECEPTOR GB2.	0.00e+00
1255	32.7	122.1	5	097133	BCDNA.GH0712.	0.00e+00
690	24.5	812	11	092308	GABAB RECEPTOR ID.	0.00e+00
691	24.5	833	11	092915	573K1.1.4 (GAMMA-AMINO	0.00e+00
695	24.5	844	5	096022	GABA-B RECEPTOR, SUBUNI	0.00e+00
691	24.5	844	11	098217	573K1.1.2 (GAMMA-AMINO	0.00e+00
690	24.5	844	11	088621	GABA-BR1 RECEPTOR.	0.00e+00
687	24.4	899	4	095975	GABAB RECEPTOR, SUBUNI	0.00e+00
682	24.4	930	4	095468	GABAB RECEPTOR, SUBUNI	0.00e+00
683	24.4	960	11	092918	CABABR1 PROTEIN.	0.00e+00
682	24.4	960	11	008620	573K1.1.1 (GAMMA-AMINO	0.00e+00
687	24.4	961	4	095375	GABA-BR1A RECEPTOR.	0.00e+00
681	24.3	960	11	092948	GABA-B1A RECEPTOR.	0.00e+00
360	19.7	662	11	092916	573K1.1.3 (GAMMA-AMINO	0.00e+00
359	19.7	875	11	092909	GABAB RECEPTOR 1C.	3.57e-24
350	19.6	241	4	075975	GABA-B RECEPTOR SPLIC	3.02e-24
367	19.6	991	11	075974	GABAB RECEPTOR SUBTYPE	1.84e-24
167	16.9	182	4	075974	GABAB RECEPTOR SPLIC	3.44e-20
167	16.9	182	4	075974	GABAB RECEPTOR SPLIC	3.44e-20
122	10.5	402	5	023442	COSMID ZK180.	1.07e-11

[illegible]


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QY 781 NOASTSRLEGLQSENHRLRMKITELDKDELEVTMQLODPTREKTYIKONHYGELNDILNL 840
Db 840 GNFTESTDGGKAILKNHLDONPOLDMNTTEPRTCKDPEDINSEPHIORSLDPLIH 899
QY 841 GNFTESTDGGKAILKNHLDONPOLDMNTTEPRTCKDPEDINSEPHIORSLDPLIH 900
Db 900 HAYLPISIGVDASCVPSPASPRHRHVRPSPFRVMSGL 940
QY 901 HAYLPISIGVDASCVPSPASPRHRHVRPSPFRVMSGL 941

RESULT 3
ID 09Y133 PRELIMINARY; PRT: 1221 AA.
AC 09Y133:
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE BCDNA.GH07312.
GN BCDNA.GH07312.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RA RUBIN G.M., WAN K.H., HARVEY D., LEWIS S.E., BROKSTEIN P., TSANG G.,
RA AGGARWANI A., ARCAINA T.T., BAXTER E., BLAZED R.G., BOTENHOFF C.,
RA CHAPE M., CHAVEZ C., CHEW M., DOYLE C.M., FARAN D.E., FRIS E.,
RA GALLE R., GEORGE R.A., HARRIS N.L., HOSKINS R.A., EVANS-HOLM M.,
RA HOUSTON K.A., HUMMASTI S.R., KIM E., LI P., MOSHREFI M., PACLEB J.M.,
RA PARK S., SEQUEIRA A., SETHI H., SNIR E., SVIRSKAS R.R., WEINBURG T.,
RA CELINKER S.E.;
RT "Full length Drosophila melanogaster cDNA sequence.";
RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF145639; AAD38614.1;
SQ SEQUENCE 1221 AA; 138124 MW; CE3B7865 CRC32;

Query Match 32.7%; Score 2255; DB 5; Length 1221;
Best Local Similarity 41.8%; Pred. No. 0.00e+00;
Matches 325; Conservative 196; Mismatches 236; Indels 21; Gaps 17;

Db 18 M5TAGCRATKASD-VYIAGFPYGDGVENSYTGRCVMPSPKALGHVNHGKILANRYLH 76
QY 42 WARGAPRPPSSPLSINKIMPLTEKVAKGISGRGLVLAELAIQIRNES-LLRPYLD 100
Db 77 MMWMDTQCAAVGVSFEDMHSKPNKVMYLFSACTHTDPIAKASKMHMLTQLSYADTH 136
QY 101 LRLYTECDNAKGLKAFYDAIKYGRPHMLVFGVCPSVTSIIAESLQGMNLVOLSFATY 160
Db 137 PMFT-KDAEPNFRVPSNAPNARLALKEFNTRVGTQYONPRPSLPHNHVADLD 195
QY 161 PVALAKKKKYPERFRVPSNAPNAPALILKLKHVOMKRVGTLODVRSEVNDLGTLY 220
Db 196 AMEVEVETQSFVNDVAESLKLREKDVRIILGNFNEHARFARFCAVKLMDYGRATOML 255
QY 221 GEDIEISDESNDPCTSVKLLKGNDAVRIILGQFDONAAKAVFCCATENNYSKTYOI 280
Db 256 IMATYSTDMN-V-TQ-DSE-CSVEIATALEGAILVDLPLTSGDITVAGITADEVYL 311
QY 281 IGWEPSPWMEQVHTEANSRCLRNLLAAMEGYIGVDEPLSSNOIKTISKTPQOYER 340
Db 312 EYDRLR-GTEYSRPHGYTYDGTMA-A-AL--AIQYV-AEKREDLLTHEDYRKDMESFVL 365
QY 341 ELVNKKSGVSPKFGYAYDGIWIAKTLQRAMETLHASSRHQRIODENYTHHTGRILL 400
Db 366 EALRNTSEFGVGPVRFVYNNERKANLLINQFOLGMEKIGEYHSQSHDLSIGKPVKW 425
QY 401 NMANENFNGVIGQVYFNGERGGITKTFQODSRKVGKGEYNAVAADLET-INDTIRQ 459
Db 426 GTPPKDRTLLIYEHQVNPITYIVSASAVIGVIAATVLAFTKYNRQRYIKMSSPHL 485
QY 460 GSEPPDKTILLIQLRKISLPLYSILSATLIIIGIMASAFLEPFNKKNNRQKIKKSSPYM 519
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Db 486 NNLIVGOMMYLSTIFLGADPTLSSVAAPPYICTARAWIIMGFSLFGAMFSKTRVH 545
QY 520 NNLIIIGMLSTYASIFLEGDSFVSEKTEETLCTYTWIIVGYTAFAGMAKTRVH 579
Db 546 SIPTDLKINKKVIKIDYOLFVWVGLAIDAIIITWOIADPEYRETKOLPLHEND-D 604
QY 580 AIFNKKKKKIIINDQKLVIYVGMLLIDLCILCQWAVDPL-RRYEXKSMEDPDGRD 638
Db 605 VLVIPENYCOSEHMTFIVSTIYAYKGLLVGAFVLAETHRAHSIPALNDSKHIGSVYN 664
QY 639 ISIRPLEHCENFTMTWIGIVAYKGLMLFGCFLMETRRNVSIPALNDSKHIGSVYN 698
Db 665 VEITCIGAATISLVSBRKDLVFLISPFITCTATLCVFPVKLVELKRNPGVV-DK 723
QY 699 VGIMCTIGAAVSFLTRDPNPVOCIALVITFCSTITLCVLPVKLITLKRNPDAQNR 758
Db 724 RVKATLRPMKNGRRDSSVCELEQ----RLDVKNTNCRFRKALMEKENELQALIRKL 777
QY 759 RFQFTQNGKREDSKTSVTSVNOASTSRLEGLQSENHRLRMKITELDKDELEVTMQLO 816

RESULT 4
ID 09Z308 PRELIMINARY; PRT: 812 AA.
AC 09Z308:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE GABAB RECEPTOR ID.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=CEREBELLUM;
RC MEDLINE; 99092370.
RA ISOMOTO S., KAIKARA M., SAKURAI-YAMASHITA Y., NAGAYAMA Y., UZONO Y.,
RA YANO K., TANIYAMA K.;
RT "Cloning and tissue distribution of novel splice variants of the rat
RT GABAB receptor.";
RL Biochem. Biophys. Res. Commun. 253:10-15(1998).
DR EMBL; AB016161; BAA34709.1;
KW Receptor.
SQ SEQUENCE 812 AA; 90920 MW; 566BF90A CRC32;

Query Match 24.5%; Score 1690; DB 11; Length 812;
Best Local Similarity 35.4%; Pred. No. 0.00e+00;
Matches 268; Conservative 194; Mismatches 271; Indels 23; Gaps 21;

Db 2 GPGGCTPVGMPLPULLVMAGVAPVMASSHPLPRPHRPVPHPSSEBRAVYIGAL-FP 60
QY 11 GPPPPPPPPARLLLLLLPL-LPL-APGAMGNARCAPR-PP-PSSPPVLSI-MGLMPLT 65
Db 61 MSGGPP-GQACPAVEALMEDVNSRDLIDPEYELKLHHSKCDPQCATKYLEYELLND 119
QY 66 KEVAKSGISGRVLAVELAIQIRNE-SLRPYLDRLYDTECDNAKGLKAFDAIKYG 124
Db 120 PIKTIIMPQ-CSSVSTVLAEARMMNLIVSYSSSPALSNRQFPFFFTPTSPATLANP 178
QY 125 PNHLLVFGVCPVSTSIIESLQGMNLVOLSFATTPVLDAKKKYPERFRVPSDNAVNP 184
Db 179 TRVLFEXMKKKKATATQOTTEVFTSTIIDLLEEVYKENGITITRTQSPFSPRAVPYNL 238
QY 185 AILKLKHVOMKRVGTLODVRSEVANDLTGLVYGEDIEISDTEFSNDPCTSVKLLK 244
Db 239 RODARIIYGLFYETEARVCEVYKERLFGKKYWPFLIGVADAMP-KTY-DP-SINCTV 295
QY 245 GNDVRIIIGQDQONMAAVFPCCATENNYSKTYMIIPGWEPSPWQVHTEANSRCLR 304
Db 296 EEMTEAVEGHITTEIVMLNPANTRISINMSTQEFVEKRLKLRKHHPETGGQFQAPLAYD 355
QY 305 KNLLAAMEGYIGVDEPLSSKOIKTISKTPQOY-EREYNN-KRSGVGPSKFH-G-YAID 360
Db 356 AIALALALANKTSG--GGRSGVLEDPFNYNNOITTDQIYAAHSSSFEGVSGHYVDAS 413
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Qy	361	GIWIAKTLQRMETLHASSRHOXIODENYTDHILGRITIANAMETFEVYGOVAF--RN	4199
Db	414	GSRAAWTLIEOLQGSYKAKIGYDYSTDDLSIW--SKTRKWIIGSGSPAQUTVIKTRFRLSQ	4722
Qy	420	GERMOTIKFTQGFQDSREKVEGEYNAVADLTIEINDTIRFGSGSEPKKTIILBQLKRISL	4799
Db	473	KLFIYSVYLSLGIYILAVNCSEFIYNSHVAYIONSQPNLNLTAVCCSIALAAVPIGL	5322
Qy	480	PLYSLSLTLTGIMMASAFLEFKIRKNQKLIMKSSPYNNKLIILGIMSLVASYISLFIPLGL	5399
Db	533	DGYHIGRQSPFVVOCARLMLLGLFSGSYGSMPIKIMVWTVFTRKEEKEWKRTELEPMK	5922
Qy	540	DGSFSEKTEFETLCYRMIWLTIVGYTTAFGAMFEKTRVHAIF--KNVKKK-KKIIIDQK	5966
Db	593	LYAYVGLLVGMDVLTLAIWQIVDPILHRTIEFLAKEEPRKEDIDVSLIPQLEHSSKKMNTW	6522
Qy	597	LLVTVGGMLLIDLCITLICQWAVDLRRTVEKYSNEPPDAGDISIRPLEHCENTHMTIW	6566
Db	653	LGIIFYGKGLLLLGIFLAYETKESVSTEKINDHRKAMATYANNAVLCILTAPYTMISSQ	7122
Qy	657	LGIYAYAYGLMLTGCFIAMETRNANVSIPALNDSKXIIGMSYANGVIMCITIGAAVSFLTRDQ	7166
Db	713	QDAAFAPASLAIIVSSYTTLVAVFVPMKRLITRGE	748
Qy	717	PNVOFCIALAVTIFCSTTLCIOLVAFPLILTRFMPD	752

RESULT	5	PRELIMINARY;	PRT;	833 AA.
TD	Q9WV15			
AC	Q9WV15;			
DT	01-NOV-1999	(TREMBLref. 12, Created)		
DT	01-NOV-1999	(TREMBLref. 12, Last sequence update)		
DT	01-NOV-1999	(TREMBLref. 12, Last annotation update)		
DE	573K1.1.4	(GAMMA-AMINOBUTYRIC ACID (GABA) B RECEPTOR, 1D).		
GN	573K1.1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	[1]			
RP	SEQUENCE FROM N.A.			
RA	YOUNGER R.;			
RL	Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AL078630; CAB44993.1; -			
KW	Receptor.			
NC	SEQUENCE 833 AA; 93167 MW; 0C07A359 CRC32;			

Query Match	24.5%;	Score 1691;	DB 11;	length 833;
Best Local Similarity	35.4%;	Pred. No. 0.00e+00;		
Matches	268;	Conservative 194;	Mismatches 271;	Indels 23;
				Gaps 21

[illegible]

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0Y      305 KNLNLAAMEGYGVDEPLEPLSSKQIKTISGKTPOOY--EREYNN-KRSGVPSKFH-G-YAYD 360
Db      356 AWMALALANKTSOG--GGRSGLVELEPENNNTITQDIYRAMSSSEFGSHVVDAS 413
QY      361 GIVWIAKTLORAMETLHAASSHRQIODEPNYTDHYLIILNAMENEFEGVOYVF-RN 419
Db      414 GSRMAMTLIEOLOGGSYKYKIYGYSTKDLSM-SKTOKWIGSPADOTLVITPFRLSO 472
QY      420 GERMTIKFTOPODSREKVKEYEYNAVADTEIIDNTRIIFGOSSEPDKDTIILOLRKISL 479
Db      473 KLEITSVSLSIGIVLAVVCSEFNINYSHVARYIONSONPINLTAVAGCSLALAVERPLG 532
QY      480 PLYSTLSMLTIIGMIIMSAFLFNFNIKRNQKLIMSSPYANNLLIJGMLSYASIFELGL 539
Db      533 DGHNGRSQSFPPVCOARLMILLGLFSSLGSGSMFKRIWVVHTVTFTKEKKEMWKTELEPK 592
QY      540 DGSEFSKTFEFLICTVRMWILTGVYTATAFGAMFAKTRVAHF--KNVKMK-KKIIKDK 596
Db      593 LRYAVGLLVAMDILTLAIWOIVDPDLHRTIEFAKEBPKEIDIVSILPOLFHSCSKMMTW 652
QY      597 LLVIYGMGLIDLCLICLCQAWDELRLRTVEKYSMEPDPAGRDISIRPLEHCENTHMWT 656
Db      653 LGIFPGYGLLLLLIGIPLAYTKSVSTEKINDRAVCAALRYNAVVLCLTPATYMLISSO 712
QY      657 LGIYVAYGGLMLGCGCFIAMETRNVNSIPALDSKYIGMSYVNGVICMICIGAASFLLRDQ 716
Db      713 QDAAFAPASLAIWFSSYITLVLPVPKMRRLITIGE 748
QY      717 PNVOFCIALVIFCSTYTCCLVPEPKLILRLRPD 752

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RESULT	ID	6	PRELIMINARY;	PRT;	844	AA.
AC	096022;					
AC	096022;					
DT	01-MAY-1999	(TIREMBLrel. 10, Created)				
DT	01-MAY-1999	(TIREMBLrel. 10, Last sequence update)				
DT	01-MAY-1999	(TIREMBLrel. 10, Last annotation update)				
DE	GABAB RECEPTOR, SUBUNIT 1B, PRECURSOR.					
GN	GABAB-R1 OR GABA-B R1B OR GABBR1.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Mammalia;					
OC	Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=CEREBELLUM;					
RC	WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,					
RA	BARNES A.A., EMSON P., FOORD S.M., MARSHALL F.H.;					
RT	"Heterodimerisation is required to form a functional GABAB receptor."					
RL	submitted (OCT-1998) to the EMBL/GenBank/DBD databases.					
RN	[2]					

RP SEQUENCE FROM N.A.
RC TISSUE=CEREELLUM;
EX MEDLINE; 99061981.
RA KAIJPMANN K., SCHULER V., MOSBACHER J., BISCHOFF S., BITT
RA HEID J., FROESTL W., LEONHARD S., PFAFF T., KARSCHIN A.,
RT "Human gamma-aminobutyric acid type B receptors are differentially
RT expressed and regulate inwardly rectifying K+ channels." *Proc. Natl. Acad. Sci. U.S.A.* 95:14991-14996(1998).
RL [3]
RN
RP SEQUENCE FROM N.A.
RA YOUNGER R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases
DR EMBL; AJ012186; CAA05940.1; -
DR EMBL; AJ225029; CAA1360.1; -
DR EMBL; AL031983; CAA21454.1; -
KW Signal; Receptor.
FT SIGNAL 1 29
FT CHAIN 30 844
FT SEQUENCE 844 AA; 95148 MW; C7342877 CRC32; POTENTIAL.
GABAR RECEPTOR, SUBUNIT 1B.

Query Match	24.5%;	Score 1695;	DB 4;	Length 844;
Best Local Similarity	35.5%;	Pred. No. 0.00e+00;		
Matches	255;	Conservative	192;	Mismatches 253;
			Indels	19;
			Gaps	17;


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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR:
RA PPAF T., MALITSCHER B., KAUFMANN K., BETTLER B., KARSCHIN K.,
RT "Alternative splicing generates a novel isoform of the rat
   metabotropic GABAB receptor."
RL Eur. J. Neurosci. 0:0(1999).
DR EMBL: Y10370; CAAT139.1; -.
DR EMBL: AF110797; AAD19657.1; -.
DR EMBL: AF110796; AAD19657.1; JOINED.
DR PFM: PFM0003; 7tm3; 1.
DR PFM: PFM01094; ANF_receptor; 1.
SQ SEQUENCE 844 AA; 95037 MW; 6611F68D CRC32;

Query Match
Best local similarity 35.4%; Score 1690; DB 11; Length 844;
Matches 268; Conservative 194; Mismatches 271; Indels 23; Gaps 21;

Db 2 GPGGCPFPVGPPLPLLVMAAGVAVPMASHSPHLPRPRPRVPPSPSSRRVYIGAL-FP 60
Oy 11 GPPPPPPPPARLLLLLLPL-LPL-ARGAMGAKRGR-P-PSSPPSLI-MGLMPLT 65
Db 61 MSGMPG-GQACQPAVEMALEDVNSRRDILPDYELKLIHDSKCDPGQATKYELLYND 119
Oy 66 KEVAKGSGRGVLPVLAELAIQIRNE-SILRPYFLDLRLYTECDNAKGLKAFYDAIKYG 124
Db 120 PIKTIIMP-GSSVTIYAERAMNLIIVSYGSSSPALSNROFPFFPFRTHPSATLHP 178
Oy 125 PNHLMVGGVCPVSTIASELQGMNLVOLSFATTPVLADKKYPYFFRTVPSDNAVNP 184
Db 179 TRVLFKMGWKIATIQOTEVETSTLDDLEERVKAGIEITRPSGSPDPAPVKNLK 238
Oy 185 AILKLKHKYKRGITLQDQKRSSEVRNDLTGLVGEDIEIDTESFSNDPCSYAKKL 244
Db 239 RODARIIVGLFETEARKEVCEYKERLFGKKYVWFLIGWADNWF-KTY-DP-SINCTV 295
Oy 245 GNDRIILIGFDQMAKAVFCACAEENMYGSKYQWIIIPGWEPSPMDQVTEANSSRCLR 304
Db 296 EEMTEAVGHTTEIVMLNPANTRSISNMTSOEFVEKTLRKRHPBEFGQCAPLAYD 355
Oy 305 KNLLAAHEGIVGDFEPLSSKQIKTISGKTPQOY-EREYNN-KRSGVPSKRFH-G-YAYD 360
Db 356 AIMALALALNKTSGG--GGRSGVRLDEDFNYNNQITTDQIYRAMNSSSFEVSGHYVDAS 413
Oy 361 GIWIAIATLQRAMETLHASSRHQRIDQFNTDHTLGRILIANMNETNFEVYGOVVF-RN 419
Db 414 GSRMAWTLIDQLGGSTKKIGYDSTKDLSW-SKTDKWTGGSPPADQVLVITFRFLSQ 472
Oy 420 GERGRTKFTQFODSRREVKGVEYNAVADTLEIINDTIRFQSGSEPPKDKTILIQLRKISL 479
Db 473 KLFTSVLSLGLIVAVVCLSPNINSHRYIIONSPNINLTAVCCSLAALAVPGL 532
Oy 480 PLYLLEALITLGMIMASAFLEFNKRNCKLTKMSSPYNNNLTILGMLSYASIFLGL 539
Db 533 DGHIHGSQEPFVCOARLMLGLGSLGYSMEFTKIMWVTVFTKKEEKEMKTELEPMK 592
Oy 540 DGSPVSEKTEFETICTVATWLTLYGTATGAMFAKTMRYHAIF--KNVMKK-KIILKDK 596
Db 593 LYATVGLVGMVLTIAIWOIVDPLHRTIETFAKEPKEDIVSILPOLHSSSKRMNTW 652
Oy 597 LVIYVGMILLIDICILCMQAVDPLRRTVEKYSMEPDPAGRIDISIRPLEHCENHTW 656
Db 653 LGIFYGKGLLLGLIFLAETKSYSTEKINDHRAVGMATYNAVCLITAPYTMILSSQ 712
Oy 657 LGIYVAKGLMLFGCLAMETKNVSIPLANDSKYIGMSYVNWICIIIGAASFLTRDQ 716
Db 713 QDAAFAPASIAIVSSYITLVLEVPKMRLLTRGE 748
Oy 717 PNVOFCIVALVITFCSTITLCLVFPVKLITLRINPD 752
RESULT 9

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ID 095975 PRELIMINARY; PRT; 899 AA.
AC 095975;
DT 01-MAY-1999 (TRENBLREL, 10, Created)
DT 01-MAY-1999 (TRENBLREL, 10, last sequence update)
DT 01-MAY-1999 (TRENBLREL, 10, last annotation update)
DE GABAB RECEPTOR, SUBUNIT 1C PRECURSOR.
GN GABAB-R1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Buthiria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RA WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,
RA BARNES A.A., EMSON P., FOORD S.M., MARSHALL F.H.;
RT "Heterodimerisation is required to form a functional GABAB receptor."
RL Submitted (OCU-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: A012187; CAA09941.1; -.
KW Signal; Receptor.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 899 GABAB RECEPTOR, SUBUNIT 1C.
SQ SEQUENCE 899 AA; 101551 MW; 04619FDC CRC32;

Query Match
Best local similarity 36.2%; Score 1687; DB 4; Length 899;
Matches 249; Conservative 180; Mismatches 243; Indels 16; Gaps 14;

Db 123 GQACQPAVEMALEDVNSRRDILPDYELKLIHDSKCDPGQATKYELLYNDPIKIIMP 182
Oy 74 GRGVLPAVELAIQIRNE-SILRPYFLDLRLYTECDNAKGLKAFYDAIKYGNLMLVFG 132
Db 183 G-CSSVTIYAERAMNLIIVSYGSSSPALSNROFPFFPFRTHPSATLHPTRVLFK 241
Oy 133 GVCPSVTIILASLQGMNLVOLSFATTPVLADKKYPYFFRTVPSDNAVNPAILKLKH 192
Db 242 WGWKRIATIQOTEVETSTLDDLEERVKAGIEITRPSGSPDPAPVKNLKRODARIIV 301
Oy 193 YOKKRGITLQDQKRSSEVRNDLTGLVGEDIEIDTESFSNDPCSYAKKLKNDVRIIL 252
Db 302 GLPYETEARKEVCEYKERLFGKKYVWFLIGWADNWF-KTY-DP-SINCTVDEMTAVE 358
Oy 253 GQFQDMAKAVFCACAEENMYGSKYQWIIIPGWEPSPMDQVTEANSSRCLRKNLLAME 312
Db 359 GHTEIIVMLNPANTRSISNMTSOEFVEKTLRKRHPBEFGQCAPLAYDAIHALALA 418
Oy 313 GTIGVDFEPLSSKQIKTISGKTPQOY-EREYNN-KRSGVPSKRFH-G-YAYDGIWVIAKT 368
Db 419 LNKTSGG--GGRSGVRLDEDFNYNNQITTDQIYRAMNSSSFEVSGHYVDASGSRMAYTL 476
Oy 369 LQRAMETLHASSRHQRIDQFNTDHTLGRILIANMNETNFEVYGOVVF-RNGERMGITK 427
Db 477 IDQLGGSTKKIGYDSTKDLSW-SKTDKWTGGSPPADQVLVITFRFLSQKLTISVS 535
Oy 428 FTQFODSRREVKGVEYNAVADTLEIINDTIRFQSGSEPPKDKTILIQLRKISL 487
Db 536 LSLGLIVAVVCLSPNINSHRYIIONSPNINLTAVCCSLAALAVPGLDQYHGRN 595
Oy 488 LTIIDGMIMASAFLEFNKRNCKLTKMSSPYNNNLTILGMLSYASIFLGLDPSVSEK 547
Db 596 QEPFVCOARLMLGLGSLGYSMEFTKIMWVTVFTKKEEKEMKTELEPMKLAATAGL 655
Oy 548 TFEETICTVATWLTLYGTATGAMFAKTMRYHAIF--KNVMKK-KIILKDKLVIYGM 604
Db 656 VGMVLTIAIWOIVDPLHRTIETFAKEPKEDIVSILPOLHSSSKRMNTWLGIFGYK 715
Oy 605 LTIIDICILCMQAVDPLRRTVEKYSMEPDPAGRIDISIRPLEHCENHTWIMGLIYAYK 664
Db 716 GLIILGIFLAETKSYSTEKINDHRAVGMATYNAVCLITAPYTMILSSQDAAFAPA 775
Oy 665 GLIILGIFLAETKSYSTEKINDHRAVGMATYNAVCLITAPYTMILSSQDAAFAPA 775
Db 776 SLAIVSSYITLVLEVPKMRLLTRGE 803

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Sun Apr 23 09:55:05 2000

US-09-211-755A-47.rsp

Page 10

Dh	61	MSGWNG -GOCAPVEMALDENVRSDRIIDPELTELHHSKCPQCATYELLYND	119
Dh	66	KEVAKSISGRVLPRAVELAIQJIRNE -SLRPFIDLRILYDECNMAGLKAFFDAIKYG	124
Dh	120	PIKILIMPQ -CSSVSTLVAEARMNLIVLSTYSSSSPALNSNOREPPTFRTHPSATLHP	178
Qy	125	PNHLMEFGVGSVYSIISAEISLOGMNIVOLSFAPATTPVLADKKYPYEFRRPDSNANVP	184
Dh	179	TRKLEKGMKRIATIOQTEVEVSTLDDLEKRVVEAGIELTFPQSEFSPAPVANKL	238
Qy	185	AILKLKHQYMKRVGLIDQVORESEVRNDLTGLVGEDIEISDPSESNPCTSHAKK	244
Dh	239	ROARITVGLFETELARRVCEVYKKEJLFGKYVWFLIGMYADNNF -KTY -DP -SINCTY	295
Qy	245	GNQVRILLQFOQNNAAKVFPCCATBENNYOSKQOIIIPQWTERSWMEOVHTEANSKCLR	304
Dh	296	EEMTEAVEGHITTEIVMLNPANTRSISNMNTSQEFVEKLYRLKRPDEETGSGOAPLAYD	355
Qy	305	KNLIAAMEGIVGDEPRLSSKOITIGSKTPQOY -BREYVN -KRSVGPSKFH -G -YAYD	360
Dh	356	AIMALALNKRISGG -GGRSGVRLPEFPNNNOITIDOLYRAMNNSSEFGSGVHYVDAS	413
Qy	361	GIWIVAKTIQRAMETLHHSKRQRIODPNTDHTLGRILNMAENETNFGYTGQVYF -RN	419
Dh	414	GSRMANTLIEOLGSGYKIKGYDYDSTKXDLISW -SKTDNMIGSGPPADOTLIVIKTFRLSQ	472
Qy	420	GERMGITKFTQFODSREKVEYENYANVADLEIINDIRFQSGSPKDXDITLIEOLRISL	479
Dh	473	KLFJASVYSSGIYLAUVACSPFNYSNHRVYONSPNINMLTAVGSLMAAIVPGL	532
Qy	480	PVSIISALTILGMIKASFLFPNKKRNQKLIKMSPPYMNMLILGMLTASITFLGL	539
Dh	533	DGHHIGRSQFPVQCARMLMLGLGFSJLGSYSPFKIWMYHIVYTKKEKKEKMKRTLEPMK	592
Qy	540	DGSSVEKFFELCTVFRWMLTVGTVTAFGAMKAKTRVNAHLE -KNVKKM -KKIIDLQK	596
Dh	593	LYATVGLGMDILTLAIQVLDYPLHRTITFPAKKEPBKEDIVSILPOLERCSKKNMTY	652
Qy	597	LTVIGMLLIDICILIGQAVDAPLRKTRVEKYSMEPDAPGRIDISTIRPLECENHTHTIW	656
Dh	653	IGELMSP 659	
Qy	657	LGIYVAY 663	

Search completed: Wed Apr 19 22:06:59 2000
Job time : 679 secs.

FT	CHAIN	34	908	MECHOTROPIC GLUTAMATE RECEPTOR 8.
FT	DOMAIN	34	583	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	584	608	I (POTENTIAL).
FT	DOMAIN	609	620	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	621	641	II (POTENTIAL).
FT	DOMAIN	642	647	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	648	668	III (POTENTIAL).
FT	DOMAIN	669	695	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	696	716	IV (POTENTIAL).
FT	DOMAIN	717	746	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	747	768	V (POTENTIAL).
FT	DOMAIN	769	781	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	782	803	VI (POTENTIAL).
FT	DOMAIN	804	818	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	819	843	VII (POTENTIAL).
FT	DOMAIN	844	908	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	95	95	POTENTIAL.
FT	CARBOHYD	298	298	POTENTIAL.
FT	CARBOHYD	452	452	POTENTIAL.
FT	CARBOHYD	480	480	POTENTIAL.
FT	CARBOHYD	565	565	POTENTIAL.
SO	SEQUENCE	908 AA;	101413 MM;	CRC32;
				255810FF

Query Match	3.58;	Score 241;	DB 1;	Length 908;
Best Local Similarity	22.18;	Pred. No. 2.61e-20;		
Matches	64;	Conservative	99;	Mismatches 101; Indels 25; Gaps 22;

[illegible]

	RESULT	2	
ID	MGR6.RAT	STANDARD:	PRT; 871 AA.
AC	P35349;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.		
GN	CRM6 OR MGLUR6.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=RETINA;		
RX	MEDLINE: 93280152.		
RA	NAKAJIMA Y., IWAKABE H., AKAZAWA C., NAWA H., SHIGEMOTO R.,		
RA	NAKASHIMI S.;		
RT	"Molecular characterization of a novel retinal metabotropic glutamate		
RT	receptor molecule with a high agonist selectivity for L-2-amino-4-		
RT	phosphonobutylate.";		
RL	J. Biol. Chem. 268:11868-11873(1993).		
CC	-1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR		
CC	IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE		
CC	ACTIVITY.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		

CC -1- TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR
CC LAYER OF THE RETINA.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC SPONGEST, TO MGLUR4.
CC -----
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CC -----

DR	EMBL: D13963; BAA03066.1; -.
DR	PIR: A46742; A46742.
DR	GCRDB; GCR_0623; -.
DR	PROSITE; PS00979; G_PROTEIN_RECPE_F3_1; 1.
DR	PROSITE; PS00980; G_PROTEIN_RECPE_F3_2; 1.
DR	PROSITE; PS00981; G_PROTEIN_RECPE_F3_3; 1.
DR	PFAM; PF00003; 7tm_3; 1.
DR	PFAM; PF01094; ANF_receptor; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW	Multi-gene family; Vision.
KW	SIGNAL
FT	CHAIN
FT	1
FT	18
FT	DOMAIN
FT	19
FT	579
FT	DOMAIN
FT	580
FT	602
FT	DOMAIN
FT	603
FT	616
FT	DOMAIN
FT	617
FT	637
FT	DOMAIN
FT	638
FT	648
FT	DOMAIN
FT	649
FT	667
FT	DOMAIN
FT	668
FT	691
FT	TRANSMEM
FT	692
FT	712
FT	DOMAIN
FT	713
FT	742
FT	TRANSMEM
FT	743
FT	764
FT	DOMAIN
FT	765
FT	777
FT	TRANSMEM
FT	778
FT	800
FT	DOMAIN
FT	801
FT	813
FT	TRANSMEM
FT	814
FT	839
FT	DOMAIN
FT	840
FT	290
FT	CARBOHYD
FT	290
FT	CARBOHYD
FT	445
FT	CARBOHYD
FT	473
FT	CARBOHYD
FT	561
FT	SEQUENCE
FT	871 AA; 95089 MW; 81A229E4 CRC32;

Query Match	Best Local Similarity	22.94%	Score 236, DB 1	Length 871
Matches	64	Conservative	90	Mismatches 102, Indels 24, Gaps 21

Db	586	LAVIG-IMATTTIMATFMHRNDPIPVASGRELTVLLTGIFLIYA-I-TF-L--MVAE	638
Qy	488	LTILIGMASAFLEFNIKNNOK-LIKMSPYNNMLIIIGMISVASIFLFGIDGSFVSE	546
Db	639	PC-AALCAARLLLGCTLLSTYALLTKTPRIIRIFEGGRSVTPPPISTPSQIVTFG	697
Qy	547	KTEETCTVTFWLLIVGYTTAFGAMPRKIMRVAIRFNNA--MKK-IIDOKLLIVYGS	603
Db	698	LTSLGVVYIAMIJAOPHSVID-YE-EQRTVPDEQA-RGVLK-CDMSDLST-IGCL-GY	751
Qy	604	MLLIDLCILICMGAVDPLRTVEKYSEMRPAGRDISTRLLBHCENTHMTWIGIYAV	663
Db	752	-SLILAVTC-TYVAIAKARVPETPNEAKPIGFTMYTTCIIIMLAFVPIFEETASAEKIYI	809
Qy	664	KGLIMGECFLAWEETRNVSIIP-ALNDSKYIGMSYVINGISCIIGAAYSFLTRDPQNVQC	722
Db	810	QTTLTVYSLSLASVSLGMLYVPKTYIILHPEDQVOKR	849
Qy	723	-IVALVI-I-FCSTITVLVFPKLLITLRINPDAAIONKR	759

RESULT	3	STANDARD;	PRT:	908	AA.
ID	MGR8_RAT				

[illegible]

```

FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
FT DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 608 I (POTENTIAL).
FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 621 641 II (POTENTIAL).
FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 668 III (POTENTIAL).
FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 696 716 IV (POTENTIAL).
FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 747 768 V (POTENTIAL).
FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 803 VI (POTENTIAL).
FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 95 95 POTENTIAL.
FT CARBOHYD 298 298 POTENTIAL.
FT CARBOHYD 452 452 POTENTIAL.
FT CARBOHYD 480 480 POTENTIAL.
FT CARBOHYD 565 565 POTENTIAL.
FT CARBOHYD 194 194 R -> A (IN REF. 2).
FT CONFLICT 460 460 T -> I (IN REF. 2).
FT CONFLICT 642 642 A -> G (IN REF. 2).
FT CONFLICT 768 768 N -> I (IN REF. 2).
FT CONFLICT 904 904 S -> T (IN REF. 2).
SQ SEQUENCE 908 AA; 101741 MM; 18865CQF CRC32;

```

Query Match 3.4%; Score 232; DB 1; Length 908;

Best Local Similarity 23.0%; Pred. No. 9,25e-19; Mismatches 98; Indels 24; Gaps 21;

Matches 65; Conservative

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Db 590 VALIGII-ATTFYIVFVRNDPIYRASGRELIVLIGIFLCYSITPLM-I-AA--PD 644
QY 488 LTLIGIMASAFLEFN-IKRNQKLIKMSPPYNNLLIIGMISTYASIFLFGDGSFVEB 546
Db 645 -TI--TCSFRRVLGLCMSTYALTKTRIRIFEOGKSKSTAKFISPAQIVITFS 701
QY 547 KTFETLTCTVETWILVGYTTFAGFMFAKTWRVHAIFKNVKK-K--KLIKDKLVIYVG 603
Db 702 LISVOLGIVFVFWVDPEHIID-YG-EORTLPEKA-RGVLR-CDISDLSL-IGSL-GY 755
QY 604 MLTDLCTILICWADVPLKRTVEKSMRPPAGRDISIRLLEHCENTHMTWLGIVYAK 663
Db 756 SILIMV-TCTVYANKTRGV-ETFENAKPIGFTWYTCIILAFIPFEGTAQSAEKMYI 813
QY 664 KGLMLFGCFL-AMETRNVSIPALNDSKYIGMSYVNGIMCIIGAIVSFLTRDPNVQFC 722
Db 814 QTTTLIVSLSASVSLGMLYPRVYIIIFHPEDNOKRRSF 856
QY 723 -IVALVI-I-FCSITTLCLVFPRLTLRTNPDAATQNRKRF 762

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RESULT 5 STANDARD; PRT; 877 AA.
AC MG6_HUMAN
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
CN GRM6 OR MGUR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97358610.
RA HASHIMOTO T., INAZAMA J., OKAMOTO N., TAGAMA Y., BESSHO Y., HONDA Y.,
RA NAKANISHI S.:
RT "The whole nucleotide sequence and chromosomal localization of the
RT gene for human metabotropic glutamate receptor subtype 6."
RL Eur. J. Neurosci. 9:1226-1235(1997).

```

```

CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGUR4.
CC -----
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CC -----
DR EMBL; U82083; AAB82068.1; -.
DR GCDRDB; GCR_2607; -.
DR MIM; 604096; -.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PIRAM; PF01094; ANF_receptor; 1.
DR G-protein coupled receptor; Transmembrane; glycoprotein; Signal;
KW Multigene family; Vision.
FT SIGNAL 1 24
FT CHAIN 25 877
FT DOMAIN 25 585
FT TRANSMEM 586 608
FT DOMAIN 609 622
FT TRANSMEM 623 643
FT DOMAIN 644 654
FT TRANSMEM 655 673
FT DOMAIN 674 697
FT TRANSMEM 698 718
FT DOMAIN 719 748
FT TRANSMEM 749 770
FT DOMAIN 771 783
FT TRANSMEM 784 806
FT DOMAIN 807 819
FT TRANSMEM 820 845
FT DOMAIN 846 877
FT CARBOHYD 296 296
FT CARBOHYD 451 451
FT CARBOHYD 479 479
FT CARBOHYD 567 567
SQ SEQUENCE 877 AA; 95436 MM; D5A6C038 CRC32;

```

Query Match 3.3%; Score 225; DB 1; Length 877;

Best Local Similarity 21.5%; Pred. No. 1.44e-17; Mismatches 106; Indels 22; Gaps 19;

Matches 60; Conservative

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Db 592 LAVLGIVATTVVAFVRNNTPIYRASGRELIVLIGIFLIYA-I-TF-L---MVAEP 645
QY 488 LTLIGIMASAFLEFNIKRNQKLIKMSPPYNNLLIIGMISTYASIFLFGDGSFVEK 547
Db 646 G-AAVCAARLFLGLTTSYSALLTKTRIRYIFEOGKRSVTPPFISSQIVITFS 704
QY 548 TPEETLCTVETWILVGYTTFAGFMFAKTWRVHAIFKNV-K-KRK-IKDKLVIYVGM 604
Db 705 TSLQVGMTAMTGARPHSVID-YE-EORTVPEQA-RGVLR-CMDSLSL-IGSL-GY 757
QY 605 ILTDLCTILICWADVPLKRTVEKSMRPPAGRDISIRLLEHCENTHMTWLGIVYAK 664
Db 758 SILIMVTC-TVAIKARGVPETFENAKPIGFTWYTCIILAFVPIFEGTAQSAEKIYQ 816
QY 665 GLTMLFGCELAETRNVSIP-ALNDSKYIGMSYVNGIMCIIGAIVSFLTRDPNVQFC- 722
Db 817 TTTTLVSLISASVSLGMLYPRVYIIFHPEDNOKRR 855
QY 723 IVALVI-I-FCSITTLCLVFPRLTLRTNPDAATQNR 759

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RESULT 6
ID MGRA_HUMAN STANDARD: PRT: 912 AA.
AC Q14833:
DT 01-NOV-1997 (Rel. 35, Created)
DR 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR MGLUR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthera; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RA MAKOFF A., LELCHUK R., OXER M., HARRINGTON K., EMSON P.;
RT "Molecular characterization and localization of human metabotropic
RT glutamate receptor type 4."
RL Brain Res. Mol. Brain Res. 37:239-248(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE: 98141892.
RX WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S.,
RA FLORE J., LUKIC S., RUEBEG D., LEONHARDT T., KNOEPFEL T., KUHN R.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RT 4."
RT Neuroparmacology 34:149-155(1995).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELLUM.
CC EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND
CC THALAMUS. NO EXPRESSION DETECTED IN LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
CC -----
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CC -----
DR EMBL: X80818; CAAS56784.1; -
DR EMBL: U92457; AAB51762.1; -
DR GCRDB: GCR_1891; -
DR GCRDB: GCR_2069; -
DR MIM: 604100; -
DR PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 32
FT CHAIN 1 32
FT DOMAIN 33 587
FT TRANSMEM 588 610
FT DOMAIN 611 624
FT TRANSMEM 625 645
II (POTENTIAL).

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FT DOMAIN 646 656
FT TRANSMEM 657 675
FT DOMAIN 676 699
FT TRANSMEM 700 720
FT DOMAIN 721 750
FT TRANSMEM 751 772
FT DOMAIN 773 785
FT TRANSMEM 786 808
FT DOMAIN 809 821
FT TRANSMEM 822 847
FT DOMAIN 848 912
FT CARBOHYD 98 98
FT CARBOHYD 301 301
FT CARBOHYD 454 454
FT CARBOHYD 484 484
FT CARBOHYD 569 569
SQ SEQUENCE 912 AA; 101867 MW; 740D9054 CRC32;

Query Match 3.3%; Score 228; DB 1; Length 912;
Best Local Similarity 21.6%; Pred. No. 4.46e-18;
Matches 62; Conservative 98; Mismatches 100; Indels 27; Gaps 22;

Db 588 AVLPFLAVVG-IAATLFFVITFVRVNDPIYKASGRELSTVLLAGIFLCYATFLL--M- 643
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 483 SILSA-FLTLGIMASAPLFPN-IKNRQKLIKSSPYMNNLLILGMLVSAISIFLGLD 540
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 644 ---IAEPDLGT-CSIRRLFLGLGMSISYALITNTNRIYRFEGGKSVSAFRISSAQ 699
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 541 GSFESEKTEFELCTVETWILTVGYTAFGAMFARTWVAHAFKVKV--MKR-KIKKOKL 597
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 700 LATFLSLISLD-IGICWPFVVDPSHSVVD-FQDQRTLDPR-FA-RGYLK-CDISDLSL- 753
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 598 LVIVGGLMLIDLCITIC-WQAVDPLRTVETKYSNEPDAGDISIRPLEHCENTHMTIW 656
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 754 ICLL-GYSMLLV-TC-TVAIKTGVDETFENAKPIGFTYTCIWLAFIPFPGTSQ 810
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 657 LGIVAYVGLMLRCCFLAMETRNVSIP-ALNDSKYSIGMSYNNIGMCICAAVSFLTRD 715
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 811 SADKLIYOTFTLVSVSLASVSLGMLYMPVYIILFHPEDQVPRK 857
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 716 QPNVQFC-IVALVI-I-FCSTITLCIVFVKLITLFTPDADATONRR 759
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 7
ID MGRA_RAT STANDARD: PRT: 912 AA.
AC P31423:
DT 01-JUL-1993 (Rel. 26, Created)
DR 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR MGLUR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RA MEDLINE: 92110002.
RX TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
RT "A family of metabotropic glutamate receptors."
RL Neuron 8:169-179(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RA MEDLINE: 93332699.
RX O'HARA P.J., SHEPPARD P.O., THOGERSEN H., VENEZIA D., HALDEMAN B.A.,
RA MCGRANE V., HOUAMED K.M., THOMSEN C., GILBERT T.L., MULVIHILL E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is
RT related to bacterial periplasmic binding proteins."
RL Neuron 11:41-52(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.

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DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GN GRM5 OR MGLUR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CN [1]
RN SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 92317054.
RA ABE T., SUGIHARA H., NAMA H., SHIGEMOTO R., MIZUNO N., NAKANISHI S.;
RT "Molecular characterization of a novel metabotropic glutamate
RT receptor mGLUR5 coupled to inositol phosphate/Ca2+ signal
RT transduction.";
RL J. Biol. Chem. 267:13361-13368(1992).
RN [2]
RP SEQUENCE OF 859-923 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-BRAIN;
RX MEDLINE: 93343913.
RA MINKAWI R., KATSUKI F., SUGIYAMA H.;
RT "A variant of metabotropic glutamate receptor subtype 5: an
RT evolutionally conserved insertion with no termination codon.";
RL Biochem. Biophys. Res. Commun. 194:622-627(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
CC CHLORIDE CURRENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS: 5A (SHOWN HERE) AND 5B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
CC 32 RESIDUES.
CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE
CC CENTRAL NERVOUS SYSTEM.
CC -1- MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE > IBOTENATE >
CC TRANS-1- AMINOCYCLOPENTYL-1,3-DICARBOXYLATE.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST. TO MGLUR1.
CC -----
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CC -----
DR EMBL: D10891; -; NOT_ANNOTATED_CDS.
DR EMBL: S64315; AAB27666.1; -.
DR PIR: A42916; A42916.
DR GCRDB: GCR_0444; -.
DR GCRDB: GCR_0760; -.
DR PROSITE: PS00979; G_PROTEIN_REC_P3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_REC_P3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_REC_P3_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Alternative splicing.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 1203 METABOTROPIC GLUTAMATE RECEPTOR 5.
FT DOMAIN 22 578 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 579 601 I (POTENTIAL).
FT DOMAIN 602 615 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 616 636 II (POTENTIAL).
FT DOMAIN 637 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 666 III (POTENTIAL).
FT DOMAIN 667 692 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 693 713 IV (POTENTIAL).
FT DOMAIN 714 736 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 737 758 V (POTENTIAL).
FT DOMAIN 759 771 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 772 794 VI (POTENTIAL).
FT DOMAIN 795 800 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 801 826 VII (POTENTIAL).

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FT	DOMAIN	827	1203	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	88	88	POTENTIAL.
FT	CARBOHYD	209	209	POTENTIAL.
FT	CARBOHYD	377	377	POTENTIAL.
FT	CARBOHYD	381	381	POTENTIAL.
FT	CARBOHYD	444	444	POTENTIAL.
FT	CARBOHYD	733	733	POTENTIAL.
FT	VARSPPLIC	876	907	MISSING (IN ISOFORM 5A).
SO	SEQUENCE	1203 AA;	131885 MM;	2955EA33 CRC32;

Query Match	3.1%	Score 215;	DB 1;	Length 1203;
Best Local	Similarity 28.3%;	Pred. No. 6.98e-16;		
Matches	54;	Conservative	57;	Mismatches 61;
			Indels 19;	Gaps 1

Db	565	AMSYSLVTNTRNRIARILAGSK-KKICITKKPRFMSACA-QLVIAF-TLIC--IG-IIGII 707
QY	565	TTARGAEAKTWVRHAFIKFVKKKKIKQDKLLVIGVGMLLIDLCILICQWQVPLRR 624
Db	708	VALFIMEPPDLMHDPSIRRYVILICWNTNGV-VYPLL-GYNGLLIL-SCTEFAFYTRVP 764
QY	625	VEKSMEDPDAGRI-SIRPLEHCENCTHTTWLGIVAYKGLMLFGC-FLAMETFRNS 682
Db	765	-ANNEKRYIAFTWYTCICIMLAFVPI-YFGSNYKILITMCF-S-VSL-SATVALGCM-FV 818
QY	683	IPALNDSKRYIGMSYVNGVICIIGAIVSFLTRQRPVQCIYALVYIIPSTITL-CLVFEV 741
Db	819	PKYVYIIAKPE 829
QY	742	PKLITLRTNPD 752

RESULT	11	STANDARD;	PRT;	1212 AA.
ID	MGFS_HUMAN			
AC	P41594;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-OCT-1996 (Rel. 34, last sequence update)			
DT	15-DEC-1999 (Rel. 39, last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.			
GN	GRM5 OR MGLUR5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 94197696.			
RA	MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., SUGIYAMA H.;			
RT	"A variant of metabotropic glutamate receptor subtype 5: an			
RT	evolutionally conserved insertion with no termination codon."			
RL	Biochem. Biophys. Res. Commun. 194:622-627(1993).			
CC	-1- FUNCTION. RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS			
CC	IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-			
CC	MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-			
CC	CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED			
CC	CHLORIDE CURRENT.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- ALTERNATIVE PRODUCTS: TWO ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE			
CC	PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF			
CC	32 RESIDUES.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.			
CC	STRONGEST, TO MGLUR1.			


```

Db 681 AL----IAKPTIGS-CVLORFEGIGVGFSTIYALLFTKTNISFIHSKSAQRLAYISE 735
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 538 GLDGSFSEKTEFTLCTVFTWILTVGYTAFGAMFAKTRVHAIFKNV-K-MKK-KIID 594
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 736 QSOVVTTSIAIOVLITMIMVVEP-PGT--RFYV-PDR--REV-I---LK-CKIQDMS 784
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 595 QKLVIVGMLIDLCILICWQAVDPURTVERTVYSMEPDAGDISIRPLEHCENTHMT 654
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 785 FLFSQLYN-MILITICTYAI-KTRKIP-ENFNESKFIQFTMTTCIIMLAFAPYFGTG 841
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 655 IMGLIVAYVGLMLPFCFLAMETRNVSIPALNDSKIGSVYVNGIMCIIGAAYELTR 714
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 842 NSYEVQTTLCISISLSAVALVCL-YSPRVYILVHPD 879
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 715 DQPNVQFCIVALVIFCSTITL-CLVFPVKLITLRTNPD 752
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
ID MGR2_HUMAN STANDARD: PRT: 872 AA.
AC 01416;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.
GN GRM2 OR MGLUR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
   Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95346007.
RA FLOR P.J., LINDNER K., PUTNER I., RUEGG D., LUKIC S., KNOPEL T.,
   KUHN R.;
RT "Molecular cloning, functional expression and pharmacological
   characterization of the human metabotropic glutamate receptor type
   2."
RT Eur. J. Neurosci. 7:622-629(1995).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
   MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE ACTIVITY.
   MAY MEDIATES SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN
   SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT REGIONS OF THE
   ADULT BRAIN AS WELL AS IN FETAL BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
   STRONGEST, TO MGLUR3.
CC -----
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CC -----
DR EMBL; L35318; AAA76855.1; -
DR GCRDB; GCR_1846; -
DR MIM; 604099; -
DR PROSITE; PS00979; G-PROTEIN_RECP_F3.1; 1.
DR PROSITE; PS00980; G-PROTEIN_RECP_F3.2; 1.
DR PROSITE; PS00981; G-PROTEIN_RECP_F3.3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
   Multigene family.
FT SIGNAL 1 18
FT CHAIN 1 872 METABOTROPIC GLUTAMATE RECEPTOR 2.
FT DOMAIN 19 567 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 568 590 I (POTENTIAL).
FT DOMAIN 591 604 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 605 625 II (POTENTIAL).
FT DOMAIN 626 636 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 637 655 III (POTENTIAL).
FT DOMAIN 656 679 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 680 700 IV (POTENTIAL).
FT DOMAIN 701 725 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 726 747 V (POTENTIAL).
FT DOMAIN 748 760 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 761 783 VI (POTENTIAL).
FT DOMAIN 784 793 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 794 819 VII (POTENTIAL).
FT DOMAIN 820 872 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 203 203 POTENTIAL.
FT CARBOHYD 286 286 POTENTIAL.
FT CARBOHYD 338 338 POTENTIAL.
FT CARBOHYD 402 402 POTENTIAL.
FT CARBOHYD 547 547 POTENTIAL.
SQ SEQUENCE 872 AA: 95507 MM; 9369084C CRC32;

Query Match 2.8%; Score 196; DB 1; Length 872;
Best Local Similarity 24.7%; Pred. No. 9.35e-13;
Matches 55; Conservative 68; Mismatches 78; Indels 22; Gaps 19;

Db 611 GGVFLCYCTETFLPA-KSTAVCTLRRLGLTASVCYSAITTKNRARIFGAREGAQ 669
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 532 ASIFL-FGLDGSFSEKTEFTLCTVFTWILTVGYTAFGAMFAKTRVHAIFKNV--MK 588
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 670 RRFISPAQVAVICLALISGOLIVAVMLVRA-PGT-GK-ETAPER--REV-V-TL--R 720
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 589 K-KIKDQKLVIVGMLIDLCILICWQAVDPURTVERTVYSMEPDAGDISIRPLEH 647
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 721 CNHRDASM-LGSL-AYNVLLIAL-CLVAFNTRKCP-ENFNESKFIQFTMTTCIIMLAL 776
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 648 CENTHMTIMGLIVAYVGLMLPFCFL-AMETRNVSIPALNDSKIGSVYVNGIMCIIGA 706
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 777 LPIFYTSSDYRYOTTTCMCVSVLSGSVYGLCL-PARKIHL 818
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 707 AAVSFLTRDQPNVQFCIVALVIFCSTITL-CLVFPVKLITLRTNPD 747
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
ID CYGR_ARBP STANDARD: PRT: 986 AA.
AC P11528;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RESACT RECEPTOR PRECURSOR (GUANYLATE CYCLASE) (EC 4.6.1.2).
OS Arabacia punctulata (Punctate sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
   Euechinoidea; Echinacea; Arbacoidea; Arbacoidea; Arbacoidea.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-TESTIS;
RX MEDLINE; 88316927.
RA SINGH S., LOWE D.G., THORPE D.S., RODRIGUEZ H., KUANG W.-J.,
   DANGOTT L.J., CHINKERS M., GOEDEL D.V., GABBERS D.L.;
RT "Membrane guanylate cyclase is a cell-surface receptor with homology
   to protein kinases."
RT Nature 334:708-712(1988).
RL Nature 334:708-712(1988).
CC -1- FUNCTION: IMPLICATED AS A CELL-SURFACE RECEPTOR ON SPERMATOZOA
   FOR 'REACT' A CHEMOTACTIC PEPTIDE, AND ON VARIOUS OTHER CELLS
   AS A RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE.
CC -1- CATALYTIC ACTIVITY: GTP = 3,'5'-CYCLIC GMP + PYROPHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC
   DOMAIN OF PROTEIN KINASES.
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DR EMBL: X12874; CAA31367.1; .
 DR PIR: S05480; OYURGA.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PFAM: PF00069; PKinase; 2.
 DR PFAM: PF01094; ANF_receptor; 1.
 DR Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
 KW GMP synthesis; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 986
 FT DOMAIN 22 507
 FT TRANSMEM 508 528
 FT DOMAIN 529 986
 FT DOMAIN 568 836
 FT CARBOHYD 185 185
 FT CARBOHYD 361 361
 FT CARBOHYD 410 410
 FT CARBOHYD 986 AA; 111284 MW; 68BFC466 CRC32;
 SQ SEQUENCE

Query Match 2.88; Score 195; DB 1; Length 986;
 Best Local Similarity 26.08; Pred. No. 1,366-12;
 Matches 52; Conservative 49; Mismatches 91; Indels 8; Gaps 7;

DB 2 ATTLLELLVVAWITVRSATLHNPVYINIDRGKPKLHGMTSWTNADNSGCTGPPS 61
 19 PPARLLLLPLPLPLAPGA-WGMARGAPRPPSSPPLISIMPLTKREYAKSGISGRV 77
 DB 62 AGAPPLAIOVANNDMDILHGYDINFEMVDTHCDINIGMAAISDMWKRGS-FLGYIGPGCG 119
 78 LPVAVELAEQIRNE-SLRBPFLDLRYDTECDNAKGLKAFYDAIKYGNHLMVFGGVC 136
 DB 120 CTYEGRLASALN-PPMIDYA-CDENPV-SNKEFYPTFLKTPRSQYVDLSILLIDMTW 176
 137 SV-TSIIAESQGMNLVQSFATTPVLDKPKKPYFETPSDVAVPALILKLKHQW 195
 OY 137 SV-TSIIAESQGMNLVQSFATTPVLDKPKKPYFETPSDVAVPALILKLKHQW 195
 DB 177 NQTVVVENITKRYNVENTM 196
 OY 196 KRVGTLTDVQVSEFVRNDL 215

RESULT 15
 ID MGR2_RAT STANDARD; PRT; 872 AA.
 AC P31421;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.
 GN GRM2 OR MGLUR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 92110002.
 RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
 RT Neuron 81:69-179(1992).
 RL "A family of metabotropic glutamate receptors.";
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
 CC MAY MEDATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN
 CC SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS AND PROMINENT
 CC EXPRESSION IS SEEN IN GOLGI CELLS OF THE CEREBELLUM AND SOME
 CC PARTICULAR NEURONAL CELLS IN OTHER BRAIN REGIONS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLUR3.
 CC -----
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 CC -----
 DR EMBL: M92075; -. NOT_ANNOTATED_CDS.
 DR PIR: JH0561; JH0561.
 DR HSSP: P06612; IECU.
 DR GCRDB: GCR0361; .
 DR PROSITE: PS00979; G_PROTEIN_RECPEP_F3_1; 1.
 DR PROSITE: PS00980; G_PROTEIN_RECPEP_F3_2; 1.
 DR PROSITE: PS00981; G_PROTEIN_RECPEP_F3_3; 1.
 DR PFAM: PF01094; ANF_receptor; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family.
 FT SIGNAL 1 18
 FT CHAIN 19 872
 FT DOMAIN 19 567
 FT TRANSMEM 568 590
 FT DOMAIN 591 604
 FT TRANSMEM 605 625
 FT DOMAIN 626 636
 FT TRANSMEM 637 655
 FT DOMAIN 656 679
 FT TRANSMEM 680 700
 FT DOMAIN 701 725
 FT TRANSMEM 726 747
 FT DOMAIN 748 760
 FT TRANSMEM 761 783
 FT DOMAIN 784 793
 FT TRANSMEM 794 819
 FT DOMAIN 820 872
 FT CARBOHYD 203 203
 FT CARBOHYD 286 286
 FT CARBOHYD 338 338
 FT CARBOHYD 402 402
 FT CARBOHYD 547 547
 FT CARBOHYD 872 AA; 95773 MW; C3C3467E CRC32;
 SQ SEQUENCE

Query Match 2.78; Score 189; DB 1; Length 872;
 Best Local Similarity 24.78; Pred. No. 1,256-11;
 Matches 55; Conservative 66; Mismatches 80; Indels 22; Gaps 19;

DB 611 GGVFLCYCMTFEFLA-KPSTAVCTLRRLGTAFCVCSALLTKTNRIARFGAREGAQ 669
 532 ASIFL-FELDSFVSEKTFETLCTVFTWILTVGYTAFAKPAKRWHAIFKRVK--MK 588
 DB 670 RPRFSPASOVALICLALISGOLLIVAMLVPE-PGT-GK-ETAPER--REV-V-TL--R 720
 589 K-KIINKQKLLVYIGGMLLDLCILICQWAVDPLKRTVTKYSMEFDPAGRIDISIRPLEH 647
 DB 721 CNHRDASM-IGSL-ANVLLIAL-CTLYAFKTRKCP-ENFNEAKFIFTMYTTCIIMLAF 776
 648 CENTHMTWLGIVAYAKGLMLFGCEL-AMETFNVSIPALNDSKRYIGMSVNVGIMCIG 706
 DB 777 LPPIFYTSDDRYOTTCMCVSISGSVYLGC-LPAPKHIIL 818
 OY 707 AAVSFLTDQPNVQPCIALVLIIFCSTITL-CLVFPKL-ITL 747

Search completed: Wed Apr 19 21:55:23 2000
 Job time : 219 secs.

Qy	74	GRGVLPANVELAL	EQLRNE - SLRRYEPFLDLRLRYDECONANGKAFYDAIKYGRHHLMVFG	1322	
Db	244	G-CSSVSTLVAAEARMNLVLYTSGSSSPALSNRQREPTFRHPSATLHNPTRYVKLF	FEK	302	
Qy	133	GVCPSVSTIIIESLQGNVLVOLSPAATPVADKKRYPFYFRVP	SDNNAVPA	LTKLLKH 192	
Db	303	MGWKRIATIOQTTEVFSTLDDLEERKVENGIETTFQSPFSDPAVYVKNLKRQDAITIV		365	
Qy	193	YQMKRVGLPTQDVQRESEVRNDLTGVLGEDIEIDSEFSEINDPCTSVKKIKGNDVHTIL		255	
Db	363	GLFETEARKEFYCEYKERELEGGKYVWFLGSMVADNMF - KLY -DP -SINCTVDME	TAVE	419	
Qy	253	GFQFDNMAAKAYFCCAYEENMTGSKYQWITIPWYEP	SWMEQVHTANSRCLRKULLAME	312	
Db	420	GHTTEIYMLNPANTRSISNMTSQEFYEKLTKRLKRHPETEGFQEAPLAYDAI	WALALA	479	
Qy	313	GYIGVDFEPLSSKQTKTISGKTPOQY - EREYN - N - KRSGVGSKPH - G - Y	AYDGI	IMVIATK 366	
Db	460	LNKISGG - - GGRSGVRLDEYVNNQITLTDQYLRAMNSSPFGVSGHYVPDASGR	MAWTL	537	
Qy	369	LQRAWETLHASSRHQRIDPFYTHTLGRILINAMENEFNGVGOYVF - R	NGERGTIK	427	
Db	538	IEOPGGSYKIKGYDSTKDDL - SKDDKMGSPPADQVLVTKTREFLSQKLFISV		596	
Qy	428	FTQPDSEVKYKGEYNAADLEIINDTIRQSGSEPPKDKITII	EQLRKISLPLYSLSA	487	
Db	597	LSLIGIVAAVCLSENINSHVRYIONSQPNLNLTA	VCSLAAVFPGLDGYHGRN	656	
Qy	488	LTIIIGMAASAFLEPININRQKLIKNSP	PMNNLII	GLGMLSYASIFLFLDGSFVSEK 547	
Db	657	OPPEVQARLMLLGLGSELSYGSMFTKIMWYHGTGFTKKEEKEMRKLTLEPKKI	ATATYGL	716	
Qy	548	TFETLCYRTMLITLVGYTTAGAMFAKRV	HAIF - KNYMK - K	KIKIDKLLVIYIGM 604	
Db	717	VGMDEVLTAIQIYDPLRHTLETFPAKEPKR	PDIVSILPOLEHCSRRKMTWLGIFYK	776	
Qy	605	LITDLCILICMOAVDPLKRYTEKISME	DDPRGRDITSLP	LEHCBENHMTIWLGI	VIAYIK 666
Db	777	GILLDGLIFLAEYTSKSTERKINDHRAV	GMALYVNAVLCITLTA	EVMTLSSQDAA	FAFA 836
Qy	665	GLIMLFGCEFLAMETRNVSISPLANSKYIGMS	YVNWGICII	GAAVSFLTRQ	PVWQCIY 722
Db	837	SLAIVFSSTYTLVLPFPRKRL	TRGCE	864	
Qy	725	ALVITFCSTITLCLAVEVFKLITL	RTPND	752	
RESULT	2				
ENTRY	149142	#type complete			
TITLE		metabotropic glutamate receptor 8 - mouse			
ORGANISM		#formal_name Mus musculus #common_name house mouse			
DATE		02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Sep-1998			
ACCESSIONS	149142				
REFERENCE	149142				
#authors		Duvoisin, R.M.; Zhang, C.; Ramonell, K.			
#journal		J. Neurosci. (1995) 15:3075-3083			
#title		A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb.			
#cross-references	MUID:95239344				
#accession	149142				
#status		preliminary; translated from GB/EMBL/DBJ			
#molecule_type	mRNA				
#residues	1-908	#label RES			
#cross-references	EMBL:U17252; NID:g854728; PID:g854729				
GENETICS					
#gene	mGluR8				
CLASSIFICATION		#superfamily metabotropic glutamate receptor 4			
KEYWORDS		neurotransmitter receptor			
SUMMARY		#length 908 #molecular_weight 101413 #checksum 2996			
Query Match	3.5%;	Score 241;	DB 2;	Length 908;	

Db	564	AVPEVLAIIGIT-AITFEVITFPRYNDTPYVRASGSELVLLTGIFLCYSTIFLM-I	640
Best Local Similarity	22.1%	Pred. No. 7,82e-17;	
Matches	64;	Conservative	99; Mismatches 101; Indels 25; Gaps 22;
Qy	483	SILSLM-LITLIMIMASAFLEFN-IKNRQKLIKSSPYMNNLLILGMLSYASIFLEGLD	540
Db	641	AA--PD-TI--ICSRRIFFLIGLGCFSFVALLTNTNRHRRFEFGKRSVAPKPIPSAQ	695
Qy	541	GSEVSEKTEFFELCTVIRWILTVGTTTAFGAFATWYHAFKNVKK-R-KIKRQKL	597
Db	696	LVTFEFLISVOLLGVFWFVVDP-PHTIIDYG-DQRTLDPE-NARGYLK-CDISDSL-I	750
Qy	598	LVIVGMLLDLCLILICQAVDPLRRITVEKYSMPDPDAGRDISIRPLEHCENTHMTIWL	657
Db	751	CSL-GYSLILM-TC-TVYAIKTKGVETNEAKPIGFTMYTTCIILWALPIPFQSAQS	807
Qy	658	GIVAYKGLMLFCGFLAMETRNVSIP-ALNDSKYICGMSYVNGIMCIIGAASFLTRDQ	716
Db	808	AEKMIQTTELTYSMSLSASISLGMVMPKYYIIIFHPDEQVQKRKRSF	856
Qy	717	PNVQPC-IVALVI-I-FCSITLCTLVEPKLITLRTPDATTQNRKROF	762
RESULT	3		
ENTRY	A46742	#type complete	
TITLE		metabotropic glutamate receptor, mglur6 - rat	
ORGANISM		formal.name Rattus norvegicus #common.name Norway rat	
DATE		21-Sep-1993 #sequence_revision 18-Nov-1994 #text.change 29-Jan-1999	
ACCESSIONS	A46742		
REFERENCE	A46742		
#authors		NakaJima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.	
#journal		J. Biol. Chem. (1993) 268:11868-11873	
#title		Molecular characterization of a novel retinal metabotropic glutamate receptor mglur6 with a high agonist selectivity for L-2-amino-4-phosphonobutyrate.	
#cross-references		MUDD:93280152	
#accession	A46742		
#status		preliminary	
#molecule_type		nucleic acid	
#residues		1-871 ##label NAK	
#cross-references		GB:DI3963; NID:9391856; PID:dl003572; PID:g391857	
#experimental_source		sequence extracted from NCBI backbone (NCBIN:133246, NCBIP:133250)	
CLASSIFICATION		#superfamily metabotropic glutamate receptor 4	
KEYWORDS		G protein-coupled receptor; transmembrane protein	
SUMMARY		#length 871 #molecular_weight 95088 #checksum 3942	
Query Match	3.4%;	Score 236; DB 2; Length 871;	
Best Local Similarity	22.9%;	Pred. No. 4.22e-16;	
Matches	64; Conservative	90; Mismatches 102; Indels 24; Gaps 21	
Db	586	LAVLG-IMATTITATFNRHNDTPYVRASGSELVLLTGIFLIYA-I-TF-L--WAE	638
Qy	488	LITLIMIMASAFLEFNINRQK-LIKNSPYMNNLLILGMLSYASIFLEGDSFVSE	546
Db	639	PC-AAICARRLILGTLTSSALLTNTNRYRFEFGKRSVPPPIPTSQLVTFG	697
Qy	547	KTEFFLCTVIRWILTVGTTTAFGAFATWYHAFKNV--MKK-IIRQKLLIVYG	603
Db	698	LTSLVGVVIMLGAQPHSVYD-YE-QQRTVDEQA-RGYLK-CDMSDSL-IGCL-GY	751
Qy	604	MLLIDCLILICQAVDPLRRITVEKYSMPDPDAGRDISIRPLEHCENTHMTIWMIVAY	663
Db	752	-SLIMATC-TVYAIKARGVETNEAKPIGFTMYTTCIILWALPIPFQSAQSAEKIYI	809
Qy	664	KGLMLFCGFLAMETRNVSIP-ALNDSKYICGMSYVNGIMCIIGAASFLTRDQPNVQFC	722
Db	810	QTTTLTVSLASVSLGMLVYPRKYIYVLFHPDEQVQKRK	849

QY 723 -IVALVI-I-FCSTITLCLVEVPKLTITLTNDPAATQNR 759

RESULT 4

ENTRY JH0563 #type complete

TITLE metabotropic glutamate receptor 4 precursor - rat

ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998

ACCESSIONS JH0563

REFERENCE JH0561

#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.

#journal Neuron (1992) 8:169-179

#title A family of metabotropic glutamate receptors.

#cross-references MUID:92110002

#accession JH0563

#molecule_type mRNA

#residues 1-912 #label TAN

COMMENT #experimental_source brain

CLASSIFICATION This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.

KEYWORDS #superfamily metabotropic glutamate receptor 4

G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

FEATURE

1-32

33-912

#domain signal sequence #status predicted #label SIG\

#product metabotropic glutamate receptor 4 #status predicted #label MET\

588-610

625-645

657-675

700-720

751-772

786-807

822-847

98,301,454,484,

569

#binding-site carbohydrate (Asn) (covalent) #status predicted\

621,689,695,859,

870

#binding-site phosphate (Ser) (covalent) #status predicted

SUMMARY #length 912 #molecular-weight 101818 #checksum 808

Query Match 3.3%; Score 225; DB 2; Length 912;

Best Local Similarity 22.6%; Pred. No. 1,66e-14;

Matches 65; Conservative 93; Mismatches 101; Indels 29; Gaps 23;

Db 588 AVLEPLFVAVG-IAATLFVVVTVYNDPIYKASGRELSTYVLAGIFLCYATFTL--M- 643

QY 483 SILSA-LTIIGMIMASAFLEFN-IKNRNOKLIKMSPPYNNLLIIGMLSYASIFLEGD 540

Db 644 ---IAEPDLGT-CSLRIFIFGLGMSISYALTKTRIRYIFEGKRSVASAPRFISPAQ 699

QY 541 GSFSVSEKTEFTLCTYRWILTVGTTAFGAMFAKTRVHAIFRNK--MKK-KIIRDQKL 597

Db 700 LAIT--FILISLQILGICVFWVDPSHSYVD-FQDQRTIDPR-FA-RGYLK-CDISDLSL 753

QY 598 LVIYVGMILLDLCIL-IC-WQAVDPLRRTYEKSMEDPDAGROISIRPLEHCENHMTI 655

Db 754 -ICLL-GYSMLMV-TC-TVYAIKTRGVPEFNEARPIGFTMYTCIWLAFPIPFQTS 809

QY 656 WLGIYVAYKGLMLFCGFLAMETRNVSIP-ALNDSKYIGMSYVNWGIMCIGAAVSFLR 714

Db 810 QSADKLYIQTTTLTVSSLSASVSLGMLYMPKYIILFHPDQNVPRK 857

QY 715 DQPNVQFC-IVALVI-I-FCSTITLCLVEVPKLTITLTNDPAATQNR 759

RESULT 5

ENTRY I58149 #type complete

TITLE metabotropic glutamate receptor - rat

ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change

ACCESSIONS I58149

REFERENCE I58149

#authors O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.; Haldeman, B.A.; McGrane, V.; Houamed, K.M.; Thomsen, C.; Gilbert, T.L.; Mulvihill, E.R.

#journal Neuron (1993) 11:41-52

#title The ligand-binding domain in metabotropic glutamate receptors is related to bacterial periplasmic binding proteins.

#cross-references MUID:93332699

#accession I58149

#status Preliminary; translated from GB/EMBL/DBJ

#molecule_type mRNA

#residues 1-912 #label RES

GENETICS #cross-references GB:M90518; NID:g205400; PID:g205401

CLASSIFICATION #superfamily metabotropic glutamate receptor 4

KEYWORDS neurotransmitter receptor

SUMMARY #length 912 #molecular-weight 101846 #checksum 818

Query Match 3.3%; Score 225; DB 2; Length 912;

Best Local Similarity 22.6%; Pred. No. 1,66e-14;

Matches 65; Conservative 93; Mismatches 101; Indels 29; Gaps 23;

Db 588 AVLEPLFVAVG-IAATLFVVVTVYNDPIYKASGRELSTYVLAGIFLCYATFTL--M- 643

QY 483 SILSA-LTIIGMIMASAFLEFN-IKNRNOKLIKMSPPYNNLLIIGMLSYASIFLEGD 540

Db 644 ---IAEPDLGT-CSLRIFIFGLGMSISYALTKTRIRYIFEGKRSVASAPRFISPAQ 699

QY 541 GSFSVSEKTEFTLCTYRWILTVGTTAFGAMFAKTRVHAIFRNK--MKK-KIIRDQKL 597

Db 700 LAIT--FILISLQILGICVFWVDPSHSYVD-FQDQRTIDPR-FA-RGYLK-CDISDLSL 753

QY 598 LVIYVGMILLDLCIL-IC-WQAVDPLRRTYEKSMEDPDAGROISIRPLEHCENHMTI 655

Db 754 -ICLL-GYSMLMV-TC-TVYAIKTRGVPEFNEARPIGFTMYTCIWLAFPIPFQTS 809

QY 656 WLGIYVAYKGLMLFCGFLAMETRNVSIP-ALNDSKYIGMSYVNWGIMCIGAAVSFLR 714

Db 810 QSADKLYIQTTTLTVSSLSASVSLGMLYMPKYIILFHPDQNVPRK 857

QY 715 DQPNVQFC-IVALVI-I-FCSTITLCLVEVPKLTITLTNDPAATQNR 759

RESULT 6

ENTRY A49874 #type complete

TITLE metabotropic glutamate receptor 7 - rat

ALTERNATE_NAMES metabotropic glutamate receptor mGluR7

ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Sep-1998

ACCESSIONS A49874

REFERENCE A49874

#authors Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.

#journal J. Biol. Chem. (1994) 269:1231-1236

#title Molecular characterization of a new metabotropic glutamate receptor mGluR7 couple to inhibitory cyclic AMP signal transduction.

#cross-references MUID:94117433

#accession A49874

#status Preliminary; translated from GB/EMBL/DBJ

#molecule_type mRNA

#residues 1-915 #label RES

GENETICS #cross-references GB:D16817; NID:g458728; PID:g458729

REFERENCE I57954

#authors Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.

#journal Mol. Pharmacol. (1994) 45:367-372

#title Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid-sensitive class of

Qy	625	VEKSMEDPAGRDI-SIRPLEBCEHCEHTWMTIMGLIVAYAKFGLMLFGC-FLAMETRNNVS	682
Db	765	-ANNEVEKATIAFMVYTCIIMIAFVPI-YGNSNYKIITMCF-S-VSL-SATVALGCM-FV	818
Qy	683	IPALNDSKIKGMSYVNGIMCTIGAAVSFLTRDPQPNVQFCYALVALIIFCSTITL-CLVFEV	741
Db	819	PKVYIILAKPE	829
Qy	742	PKLITLRNPD	752
RESULT	8		
ENTRY	JC2132	#type complete	
TITLE		metabotropic glutamate receptor 5 A - human	
ORGANISM		#format_name Homo sapiens #common_name man	
DATE	28-Aug-1985	#sequence_revision 07-Oct-1994	#text_change
ACCESSIONS	JC2132		
REFERENCE	JC2131		
#authors	Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.		
#journal	Biochem. Biophys. Res. Commun. (1994)	199:1136-1143	
#title	Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor subtype 5.		
#cross-references	MIMD:94197696		
#accession	JC2132		
#molecule	1-1180	#label MIN	
#residues			
COMMENT	This protein is coupled to guanine nucleotide binding proteins.		
KEYWORDS	glycoprotein; neurotransmitter; receptor; transmembrane protein		
FEATURE			
580-604	#domain transmembrane	#status predicted	#label TM1\
617-637	#domain transmembrane	#status predicted	#label TM2\
644-664	#domain transmembrane	#status predicted	#label TM3\
694-714	#domain transmembrane	#status predicted	#label TM4\
738-759	#domain transmembrane	#status predicted	#label TM5\
773-794	#domain transmembrane	#status predicted	#label TM6\
803-827	#domain transmembrane	#status predicted	#label TM7\
SUMMARY	#length 1180	#molecular_weight 129053	#checksum 237
Query Match	3.1%;	Score 215;	DB 2; Length 1180;
Best Local Similarity	28.3%;	Pred. No. 4,496-13;	
Matches	54;	Conservative 57;	Mismatches 61; Indels 19; Gaps 17;
Db	656	ANSYSLATVKTNRARIAGSK-KKICTKKRFPNSACA-QLVIAF-IILC---IQ-LGIT	708
Qy	565	TFAFGAMFKTRVIAIKFNKYNKKKIIKDKRLVLYVGMLLDLCILICQAVDPIRRT	624
Db	709	VALFTMEPRDIIHNDPSIREVYLICNTNTNLGV-VTPL-GYNGSLIL-SCFEYARFERNVP	765
Qy	625	VEKYSMEPRDGRDI-SIRPLEBCEHCEHTWMTIMGLIVAYAKGLMLFGC-FLAMETRNNVS	682
Db	766	-ANNEVEKATIAFMVYTCIIMIAFVPI-YGNSNYKIITMCF-S-VSL-SATVALGCM-FV	819
Qy	683	IPALNDSKIKGMSYVNGIMCTIGAAVSFLTRDPQPNVQFCYALVALIIFCSTITL-CLVFEV	741
Db	820	PKVYIILAKPE	830
Qy	742	PKLITLRNPD	752
RESULT	9		
ENTRY	JC2131	#type complete	
TITLE		metabotropic glutamate receptor 5 B - human	
ORGANISM		#format_name Homo sapiens #common_name man	
DATE	28-Aug-1985	#sequence_revision 07-Oct-1994	#text_change
ACCESSIONS	JC2131		
REFERENCE	JC2131		
#authors	Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.;		

Query Match	3.18;	Score 215;	DB 2;	Length 1212;
Best Local Similarity	28.38;	Pred. No. 4.49e-13;		
Matches	54;	Conservative	57;	Mismatches 61;
				Indels 19;
				Gaps 17

RESULT	10	T02740	#type complete
ENTRY		probable ligand-gated ionic channel protein T914.18 -	
TITLE		Arabidopsis thaliana	
ORGANISM		#formal_name Arabidopsis thaliana	#common_name mouse-ear cress
DATE	24-Mar-1999	#sequence_revision	24-Mar-1999
		#text_change	24-Mar-1999

Query Match	2.88;	Score 193;	DB 2;	Length 940;
Best Local Similarity	25.28;	Pred. No. 5.29e-10;		
Matches	33;	Conservative	40;	Mismatches 53;
				Indels 5;
				Gaps 4;

RESULT	11
ENTRY	OYURGA
TITLE	#type complete
ALTERNATE_NAMES	spectact receptor precursor - sea urchin (Arbacia punctulata)
CONTAINS	guanylate cyclase, membrane-bound
ORGANISM	guanylate cyclase (EC 4.6.1.2)
DATE	#formal_name Arbacia punctulata #common_name punctate urchin
	30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change

Protein	#residues	#superfamily membrane-bound guanylate cyclase; guanylate
22-37; 206-212; 280-307; 366-368, 'S', 370, 'N', 372-373, 'X'		
375-378; 549-552; 873-874, 'H', 876 #label S1N2		

FEATURE	
1-21	#domain signal sequence #status predicted #label SIG
22-986	#product quant[ate cvc]ase, membrane-bound #status

SUMMARY	PROPERTIES
#length 986	#molecular-weight 111283
	#checksum 19222
Query Match	2.88; Score 195; DB 1; Length 986;

Db 177 NOVTVENTIKYRNVFTM 196
 OY 196 KRVGLTRQDVORSEVRNDL 215

RESULT 12
 ENTRY JH0561 #type complete
 TITLE metabotropic glutamate receptor 2 precursor - rat
 ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
 DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998

ACCESSIONS JH0561
 REFERENCE JH0561
 #authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
 #journal Neuron (1992) 8:169-179
 #title A family of metabotropic glutamate receptors.
 #cross-references MUID:92110002

FEATURE 1-22
 1-18 #accession JH0561
 19-872 #molecule_type mRNA
 #residues 1-872 #label TAN
 #experimental_source brain
 COMMENT This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.
 CLASSIFICATION #superfamily metabotropic glutamate receptor 4
 KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

FEATURE 1-18
 19-872 #domain signal sequence #status predicted #label SIG
 #product metabotropic glutamate receptor 2 #status predicted #label MPT

568-590 #domain transmembrane #status predicted #label TR1\
 605-625 #domain transmembrane #status predicted #label TR1\
 637-655 #domain transmembrane #status predicted #label TR1\
 680-700 #domain transmembrane #status predicted #label TR1\
 726-747 #domain transmembrane #status predicted #label TR1\
 761-782 #domain transmembrane #status predicted #label TR1\
 795-819 #domain transmembrane #status predicted #label TR1\
 -203,286,338,402, #binding_site carbohydrate (Asn) (covalent) #status predicted\
 347
 601,675,827,837, #binding_site phosphate (Ser) (covalent) #status predicted\
 843
 832 #binding_site phosphate (Thr) (covalent) #status predicted

SUMMARY #length 872 #molecular_weight 95773 #checksum 5740

Query Match 2.7%; Score 189; DB 2; Length 872;
 Best Local Similarity 24.7%; Pred. No. 1,866-09;
 Matches 55; Conservative 66; Mismatches 80; Indels 22; Gaps 19;

Db 611 GGVFLCYMTVEFIA-KSTAVCTLRRLGTAFCVCSALLTKTNRIARFGARREGAQ 669
 OY 532 ASIFL-FGLDGSFVSEKFEFFELCTVRLWLVGYTTAGAFATKRVHALFKNVK-MK 588

Db 670 RPRFTSPASQVAICLALISGQLLYAAWLVYEA-PGT-GK-ETAPER--REV-V-TL--R 720
 OY 589 K-KIKDKQLVIVGMLIDICILICQAVDPKRRVEKYSMEDEPGRDISIRPLEH 647

Db 721 CNHRDASM-LGSL-AYNVLLIAL-CTLYAFKTRKCP-ENFNDAKPIGTWTTCIWLAF 776
 OY 648 CENNTMTTWLGLVIAVKGILMLFGCFL-AMETRNVSIPALDSKIGKISVNVGIMCITG 706

Db 777 LPIFVTSDDYRVQTTMCVSVSLSGSVVLGCL-FAPKLIITL 818
 OY 707 AAVSFLTRDQPNVQFCYALVIFCSTTL-CLVFPVKL-ITL 747

RESULT 13
 ENTRY JH0562 #type complete
 TITLE metabotropic glutamate receptor 3 precursor - rat
 ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998

ACCESSIONS JH0562
 REFERENCE JH0561
 #authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
 #journal Neuron (1992) 8:169-179
 #title A family of metabotropic glutamate receptors.
 #cross-references MUID:92110002

ACCESSION JH0562

FEATURE 1-22
 23-879 #domain signal sequence #status predicted #label SIG
 #product metabotropic glutamate receptor 3 #status predicted #label MPT

577-599 #domain transmembrane #status predicted #label TR1\
 614-634 #domain transmembrane #status predicted #label TR1\
 646-664 #domain transmembrane #status predicted #label TR1\
 689-709 #domain transmembrane #status predicted #label TR1\
 735-756 #domain transmembrane #status predicted #label TR1\
 770-791 #domain transmembrane #status predicted #label TR1\
 804-828 #domain transmembrane #status predicted #label TR1\
 209,292,414,439 #binding_site carbohydrate (Asn) (covalent) #status predicted\
 610,845 #binding_site phosphate (Ser) (covalent) #status predicted

SUMMARY #length 879 #molecular_weight 98959 #checksum 5581

Query Match 2.7%; Score 187; DB 2; Length 879;
 Best Local Similarity 34.6%; Pred. No. 3,476-09;
 Matches 28; Conservative 26; Mismatches 26; Indels 1; Gaps 1;

Db 145 VIGSSYSVSIOVANLRLRQLPQISYASATLSKRSYDYFARVPPDFQARAMEI 204
 OY 130 VFSGVCPSTVSTIAESIQGNLVLSFAATVPVLAQKKRPYFRTVPDANVPAITKL 189

Db 205 LRFENMYSTVASEGD-YGE 224
 OY 190 LKHQKRVGTLTRQDVORSE 210

RESULT 14
 ENTRY S49341 #type complete
 TITLE calcium-sensing receptor - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 03-Aug-1995

ACCESSIONS S49341; A49419; B49419; C49419
 REFERENCE S49341
 #authors Pearce, S.H.S.; Thakker, R.V.
 #submission submitted to the EMBL Data Library, August 1994
 #accession S49341
 #status preliminary

Db 721 CNHRDASM-LGSL-AYNVLLIAL-CTLYAFKTRKCP-ENFNDAKPIGTWTTCIWLAF 776
 OY 648 CENNTMTTWLGLVIAVKGILMLFGCFL-AMETRNVSIPALDSKIGKISVNVGIMCITG 706

REFERENCE #molecule_type DNA
 #residues 1-1078 #label PEA
 #cross-references EMBL:X81086
 #authors Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, T.; Seidman, C.E.; Seidman, J.G.
 #journal Cell (1993) 75:1297-1303
 #title Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalcemic hypercalcaemia and neonatal severe hyperparathyroidism.
 #cross-references MUID:94094324
 #accession A49419
 #status preliminary
 #molecule_type DNA

```
##residues      178-180,'K',182-192 ##label POL
##experimental_source family N
##note          sequence inconsistent with nucleotide translation
##note          sequence modified after extraction from NCBI backbone
##note          186-Arg mutation is associated with familial
```

```

Db      185  RTIPDEQAAAMADIIIEFFNNVYITAAD 215
          | | | | | : : : : : |
Oz      174  RTVPSDNNVNFALLKTLKHVQMKRKYITLQD 204

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Search completed: Wed Apr 19 21:51:26 2000
Job time : 96 secs.

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##note      sequence extracted from NCBI backbone (NCBI:142453)
##accession B49419
##status    preliminary
##molecule_type DNA
##residues  289-303 ##label PO2
##experimental_source family E
##note      sequence modified after extraction from NCBI backbone
##note      298-Lys mutation is associated with fami11
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##note      sequence extracted from NCBI backbone (NCBIN:142455)
accession   C49419
##status    preliminary
##molecule_type  DNA
##residues  788-802 ##label PO3
##experimental_source family J
##note      sequence modified after extraction from NCBI backbone
##note      796-TTP mutation is associated with familial
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##note      sequence extracted from NCBI backbone (NCBIN:142457)
SUMMARY     #length 1078 #molecular-weight 120672 #checksum 8159
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- Query Match	2.78;	Score 187;	DB 2;	Length 1078;
Best Local Similarity	26.48;	Pred. No. 3.47e-09;		
Matches	24;	Conservative	34;	Mismatches 33;
			Indels 0;	Gaps 0;

Db 125 LDECNCSEHIPSTIAVVGAGCGSVTAIVANLGLFYIPQVSYASSRLLSNKNQJOSFL 184
 0y 114 LKAFVDAIKYGNHLMVFGVGCPSVTSLIAESLQGMNLVQLSFAATTPVLADKKKTYFF 173

Db 185 RTIPNDEHQATAMADIIIEFRWNVGTIAAD 213
 174 RTVPSDNAVNPAILKLKLKHVQWKRVTLLTD 204

RESULT	15
ENTRY	A56715
TITLE	#type complete calcium receptor (clone pPCar-4.0) - human
ORGANISM	#formal name Homo sapiens #common name man
DATE	19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999

ACCESSIONS	A56715
REFERENCE	A56715
#authors	Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.
#journal	Brown, E.M.; Hebert, S.C.; Nemeth, E.F.; Fuller, F.
#title	Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.
#cross-references	NUID:95279439

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#accession      A56715
#status         preliminary
##residues     1-1078 ##label GAR
##molecule_type mRNA
##cross-references GB:U02075; NID:g6683744; PID:g683745
glycoprotein; receptor; transmembrane protein
#length 1078 #molecular_weight 120573 #checksum 7868
SUMMARY

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Query Match	2.78;	Score 184;	DB 2;	Length 1078;
Best Local Similarity	26.48;	Pred. No. 8.81e-09;		
Matches	24;	Conservative	34;	Mismatches 33;
			Indels 0;	Gaps 0;

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Dd      125 LDFEPCNSCHIIPTSTAIVGATGSGVSTAVALNLGFYIPQVSYSASSRLLSNKNQKPSFL 184
         | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      114 LKAIFYDAIKYPNNHLMVFGEVCPSVSIIAESLQGMLNVLQSLFAATTTPVLADKKKPYFF 173
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Db      185  RTTIDDEQAAAMADIIIEFFRNWYITGAD 215
          | | | | | | | | | | | | | | | |
Oy      174  RTVPSDNNVNFALLKTLKHNYOMKRVGTLTD 204

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Search completed: Wed Apr 19 21:51:26 2000
Job time : 96 secs.

Db 185 RTIPNDEHQATAMADIIEYFRWNVGTIAAD 215
 174 RTVPSDNAVNPAILKLKLKHQWKRVTLLTQD 204

Search completed: Wed Apr 19 21:51:26 2000
Job time : 96 secs.

CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: (206) 467-9600
CC	TELEFAX: (415) 543-5043
CC	INFORMATION FOR SEQ ID NO: 19:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 912 amino acids
CC	TYPE: AMINO ACID
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: Protein
CC	SEQUENCE 912 AA: 102014 MW: 4464621 CN:
CC	Query Match 3.3%, Score 225; DB 4; Length 912;
CC	Best Local Similarity 22.6%; Pred. No. 6,57e-07;
CC	Matches 65; Conservative 93; Mismatches 101; Indels 29; Gaps 23
Db	588 AVLPPLFAVVG-IAATLFFVVFVFNNDTPIVKASGRELSYVLGIFLCYATFP--M- 643
Qy	483 SILSA-LTILIGIMASAFLEFN-INKRQKLIKMSPTVMNLIILGMLSYASIFLPGID 540
Db	644 ---IAEDDGT-CSENRIFLGKMSISYALLTNTNRYIFRQGRKSASAPRFISPSQ 699
Qy	541 GSFVSEKTEFETICTQVFTWILLVGYTTAGCAFAKTVVHAIFKNVK--MKK-KIKDKRL 597
Db	700 LAIT--FIIISIQLGICWFVVDSSHVVO--FDDQGTIDPR-FA-RGYLK-CDISDSTL 753
Qy	598 LVIVGKMLDLCIL-TC-WQAVNDLRTVETKISMEDPPAGRODISTRPLEHCEHTHTI 655
Db	754 -ICLL-GYSMLLV--TC-TVVAIKTRGVEPEFNNAKPIGFTMYTTCIVMLAIPIFFGTS 809
Qy	656 WLGIYVAVKLMLPECFIAMETRNVSLP-ALNDSKIKGSYVNVGIMCIIGAASFLLR 714
Db	810 QSADKLIQTITLTYSVSLASVSGMLYMKRYIIILFHPQNVPRK 857
Qy	715 DQPVQFC-IVALVI-I-FCSTITCLAVEPRKILTLTPDPAQNR 759
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ID	US-08-453-862-2 STANDARD; PRT; 915 AA.
XX	xxxxxx
DE	Sequence 2, Application US/08453862
XX	Sequence 2, Application US/08453862
CC	Patent No. 5738999
CC	GENERAL INFORMATION:
CC	APPLICANT: Segerson, Thomas P.
CC	APPLICANT: Kinzie, J. Mark
CC	APPLICANT: Mulvihill, Eileen R.
CC	APPLICANT: Saugstad, Julie A.
CC	APPLICANT: Westbrook, Gary L.
CC	TITLE OR INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
CC	NUMBER OF SEQUENCES: 5
CC	CORRESPONDENCE ADDRESSES:
CC	ADDRESSEE: Townsend and Townsend and Crew LLP
CC	STREET: Two Embarcadero Center, 8th Floor
CC	CITY: San Francisco
CC	STATE: CA
CC	COUNTRY: USA
CC	ZIP: 94111-3834
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC Compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/453,862
CC	FILING DATE: 30-MAY-1995
CC	CLASSIFICATION: 436
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 08/176,401


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CC      FILING DATE: 30-DEC-1993
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Parmelee, Steven W.
CC      REGISTRATION NUMBER: 31,990
CC      REFERENCE/DOCKET NUMBER: 13952-18-2
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 206-467-9600
CC      TELEFAX: 415-576-0300
CC      INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 915 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 915 AA; 102231 MW; 4431664 CN;

Cc      Query Match          3.1%; Score 214; DB 1; Length 915;
Cc      Best Local Similarity 22.9%; Pred.No.3,81e-06;
Cc      Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22.

Dd      597 LAMIGIT-ATIFVMAPIFYNDPIYRAGSGRELSYVLITGIFCY--ITYF-L--MIA- 648
Dd      488 LTILGMIMASAFLEFN-IKNNOKLKIKSSPYNNMLIILGGMLSYSASIFLFGIDGSFVSE 546
Dd      649 KPDVAVCGRFRVFELGLGMCISYAALLTKTNLYIRHFEQKKSVAPRLISTSOLATSS 708
Dd      *   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd      547 KTFEFLCIVRFWILLTVGTTFATFGAMFAFTWVVAIFKNVKMK-K-RIKDKLLVTGG 603
Dd      709 LISVOLLEGVFI-WFGVDPPNIIID-YD-EHKTMNPDEA-RGVLK-CDITDLOI-ICSL-G 761
Dd      Oy   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Dd      604 MLILDV-CILICMOAVDPRLRTVEKYSNRPDPAGRODISIRPLEHCENTHTTILMGVIYA 662
Dd      Db  762 YSILLM-TCTYYAAIKTRGVPENEFNENAKPIGFTMYTTCIYMLAFIPFEGTAOSAEKLY 819
Dd      Oy   |||: |   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd      663 YKGILMLRGCEFLAMEPTRNVSIPA-LNDSKIYGMSYNNVGIMCIIGAAYVSFLTRDQPNVQF 721
Dd      Db  820 IOTTTLTISMNLASVALGMLYMPRYIIITHPELANOVKRKRSF 863
Dd      Oy   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
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RESULT      4
Cc      ID US-08-452-734A-2 STANDARD: PRT; 915 AA.
Cc      AC xxxxxx
Cc      DT
Cc      XX Sequence 2, Application US/08452734A
Cc      DE
Cc      XX Patent No. 5831047
Cc      CC GENERAL INFORMATION:
Cc      CC APPLICANT: Segerson, Thomas P.
Cc      CC APPLICANT: Kinzie, J. Mark
Cc      CC APPLICANT: Mulvihill, Eileen R.
Cc      CC APPLICANT: Saugstad, Julie A.
Cc      CC APPLICANT: Westbrook, Gary L.
Cc      CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
Cc      CC NUMBER OF SEQUENCES: 5
Cc      CC CORRESPONDENCE ADDRESS:
Cc      CC ADDRESSEE: Townsend and Townsend and Crew LLP
Cc      CC STREET: Two Embarcadero Center, 8th Floor
Cc      CC CITY: San Francisco
Cc      CC STATE: CA
Cc      CC COUNTRY: USA
Cc      CC ZIP: 94111-3834
Cc      CC COMPUTER READABLE FORM:
Cc      CC MEDIUM TYPE: Floppy disk
Cc      CC COMPUTER: IBM PC compatible
Cc      CC OPERATING SYSTEM: PC-DOS/MS-DOS
Cc      CC SOFTWARE: Patentin Release #1.0, Version #1.25
Cc      CC CURRENT APPLICATION DATA:
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[illegible]

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CC CC NAME: Parmelee, Steven M
CC REGISTRATION NUMBER: 31,990
CC REFERENCE/DOCKET NUMBER: 13952-18PC
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 467-9600
CC CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 915 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC CC
CC SEQUENCE 915 AA; 102231 MW; 4431664 CN;
SQ
Query Match 3.1%; Score 214; DB 4; Length 915;
Best Local Similarity 22.9%; Pred. No. 3,81e-06;
Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22.
Db 597 LAMLGIT-ATIVYMAFTIRYNDTPIVRASGRSELSVLLTGIFLCY--IITP-L---MIA- 648
QY 488 LTILGIMMSAFLFPN-IKNRQKLIKSSSPMNLLIILGMLSYASIFLGLDGSFEVS 546
Db 644 KPDVAVSRRRYFLIGACISYAALLTFRNKRIYRIFEQGKKSVAPRLIPTSLATSS 708
QY 547 KREFELCYRTMYILLVGTTAGANFATWYHAIFFKVKK-K--KIIDOKLLVIYG 603
Db 709 LISVOLLEVT-WFGVDPENIITD-YD-EHKTMNDEQA-RGVLR-CDITDLQI-ICSL-G 761
QY 604 MLIIID-CILICQOAVDELPLRTVEKYSEMPPDPAHDISIRPLEHCENTHMTWLGIYA 662
Db 762 YSILLMV-TC-IYVAKTRGVDPENNEKRPGFNYTTCIYLWLFPIFGTAOSAELY 819
QY 663 YKGLMLRGCLFAMETRWNSIPA-LNSKSYIGMSYVNWGICIIIGAASVFELTRDPNVQF 721
Db 820 IQTTLTISMNLASVALGMLYMPKYYIIIPHELINQKRKRSF 863
QY 722 C-IYALVI-I-FCSTITLCIVFPRLLITLKINPDAAIONRRFOF 762
RESULT 6 STANDARD; PRT; 879 AA.
XX AC xxxxxx
XX DE
XX DT
XX FF
XX GG
XX HH
XX II Sequence 6, Application US/08072574
XX JJ Patent No. 5521297
XX KK GENERAL INFORMATION:
XX LL APPLICANT: Daggett, Lorrie
XX MM APPLICANT: Ellis, Steven B.
XX NN APPLICANT: Liaw, Chen
XX OO APPLICANT: Pontslar, Aaron
XX PP TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,
XX QQ TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
XX RR NUMBER OF SEQUENCES: 13
XX SS CORRESPONDENCE ADDRESS:
XX TT ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
XX UU STREET: 444 South Flower Street, Suite 2000
XX VV CITY: Los Angeles
XX WW STATE: CA
XX XX COUNTRY: USA
XX YY ZIP: 00719
XX ZZ COMPUTER READABLE FORM:
CC MEDIM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/072,574
CC FILING DATE: 19930604
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CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Reiter, Stephen E.
CC REGISTRATION NUMBER: 31,192
CC REFERENCE/DOCKET NUMBER: P41 9383
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 213-622-7700
CC TELEFAX: 213-489-4210
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 879 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 879 AA; 98878 MW; 4241110 CN;
SQ

Query Match 2.7%; Score 187; DB 1; Length 879;
Best Local Similarity 34.6%; Pred. No. 2,666-04;
Matches 28; Conservatively 26; Mismatches 26; Indels 1; Gaps 1;

Db Db 145 VIGSGSSVSIOVANLRLFOIPQISVSTSAKLSDSRSDYFARTVPPEYQAKAAEI 204
Qy Qy 130 YEGVCPSPTSLIASLQGMVLVOLSFATTPPLVDKKKKYFFFRVTSPDMANVPALIKL 169
Db Db 205 LRFENMTYSVTASRGD-YGE 224
Qy Qy 190 LKHQMKRRVGLTDVDRFS 210

RESULT 7 STANDARD; PRT; 879 AA.
ID US-08-486-270-6
AC xxxxxx
DF
DE Sequence 6, Application US/08486270
XX
XX Sequence 6, Application US/08486270
XX Patent No. 5807689
CC GENERAL INFORMATION:
CC APPLICANT: Daggett, Lorrie
CC APPLICANT: Ellis, Steven B.
CC APPLICANT: Liaw, Chen
CC APPLICANT: Pontsler, Aaron
CC APPLICANT: Johnson, Edwin C.
CC APPLICANT: Hess, Stephen D.
CC TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
CC TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
CC STREET: 444 South Flower Street, Suite 2000
CC CITY: Los Angeles
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/486,270
CC FILING DATE: 02-JUN-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/072,574
CC FILING DATE: 04-JUN-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Reiter, Stephen E.
CC REGISTRATION NUMBER: 31,192
CC REFERENCE/DOCKET NUMBER: Fp41 9772
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CC      LENGTH: 879 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 879 AA; 98878 MW; 4241110 CN;

Query Match          2.7%: Score 187; DB 3; Length 879;
Best Local Similarity 34.6%; Pred. No. 2,66e-04;
Matches 26; Conservative 26; Mismatches 26; Indels 1; Gaps 1

Db
145 VIGGSYSVSIQVAMILRLFOIPQISTASTSAKLSDKSRDYFARTVPDFYQAKMAEI 204
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
OY 130 VVGVCPSVTSIIASISLGQMWLVQISFAATPTVLADKKKKYFFFTVSDNANPAIIKL 189
Db 205 LRFNWTVSYVASGCD-YGE 224
   |:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
OY 190 LKHQMKRYGTLTDVQRFSE 210

RESULT          9
ID US-08-072-574-2 STANDARD; PRT; 905 AA.
XX      xxxxxx
DT
XX
XX
DE      Sequence 2, Application US/08072574
CC      Sequence 2, Application US/08072574
CC      Patent No. 5521297
CC      GENERAL INFORMATION:
CC      APPLICANT: Daggett, Lorrie
CC      APPLICANT: Ellis, Steven B.
CC      APPLICANT: liaw, Chen
CC      APPLICANT: Pontsler, Aaron
CC      TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,
CC      TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
CC      NUMBER OF SEQUENCES: 13
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
CC      STREET: 444 South Flower Street, Suite 2000
CC      CITY: Los Angeles
CC      STATE: CA
CC      COUNTRY: USA
CC      ZIP: 00719
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/072,574
CC      FILING DATE: 19930604
CC      CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Reiter, Stephen E.
CC      REGISTRATION NUMBER: 31,192
CC      REFERENCE/DOCKET NUMBER: P41 9383
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 213-622-7700
CC      TELEFAX: 213-489-4210
CC      INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 905 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 905 AA; 101396 MW; 4448023 CN;

Query Match          2.7%: Score 189; DB 1; Length 905;
Best Local Similarity 36.1%; Pred. No. 1.95e-04;
Matches 26; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

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Db	159	VITGSSSSVAIQONVNILOPDIPOIAVASNISIDISDITLTKYFLRVVSPDTLQARMLDI	218
Qy	130	VITGSSSSVAIQONVNILOPDIPOIAVASNISIDISDITLTKYFLRVVSPDTLQARMLDI	189
Db	219	VKRYNMTVVSAY	230
Qy	190	VKRYNMTVVSAY	201
RESULT	10	STANDARD;	PRT;
ID	PCY-US91-09422-17	STANDARD;	906 AA.
XX	AC	xxxxxx	
XX	DT		
XX	Sequence 17, Application PC/TUS9109422		
CC	Sequence 17, Application PC/TUS9109422		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Multivihill, Eileen R.		
CC	APPLICANT: Hagen, Frederick S.		
CC	APPLICANT: Houamed, Khaled M.		
CC	APPLICANT: Almers, Wolfhard		
CC	TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS		
CC	NUMBER OF SEQUENCES: 33		
CC	CORRESPONDENCE ADDRESSES:		
CC	ADDRESSEE: Townsend and Townsend		
CC	STREET: One Market Plaza, Steuart Street Tower		
CC	CITY: San Francisco		
CC	STATE: California		
CC	COUNTRY: USA		
CC	ZIP: 94105-1492		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: PCY/US91/09422		
CC	FILING DATE: 19911212		
CC	CLASSIFICATION: 435		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 07/672,007		
CC	FILING DATE: 18-MAR-1991		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 07/648,481		
CC	FILING DATE: 30-JAN-1991		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 07/626,806		
CC	FILING DATE: 12-DEC-1990		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Parmelee, Steven W.		
CC	REGISTRATION NUMBER: 31,990		
CC	REFERENCE/DOCKET NUMBER: 13952-6PC		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: (206) 467-9600		
CC	TELEFAX: (415) 543-5043		
CC	INFORMATION FOR SRD ID NO: 17:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 906 amino acids		
CC	TYPE: AMINO ACID		
CC	TOPOLOGY: linear		
CC	MOLECULE TYPE: protein		
CC	SEQUENCE 906 AA; 101637 MW; 4413609 CN;		
Qy	Query Match	2.7%;	Score 186; DB 4; Length 906;
Qy	Best Local Similarity	36.1%;	Pred. No. 3.11e-04;
Qy	Matches	26; Conservative	21; Mismatches 25; Indels 0; Gaps 0;
Db	159	VITGSSSSVAIQONVNILOPDIPOIAVASNISIDISDITLTKYFLRVVSPDTLQARMLDI	218
Qy	130	VITGSSSSVAIQONVNILOPDIPOIAVASNISIDISDITLTKYFLRVVSPDTLQARMLDI	189

D	b		219 VKINMTYVSAY	230	
		: : : :			
O	y		190 LKHQMKRVGTL	201	
R	E	S	U	L	T
I	D		US-08-486-270-2		STANDARD;
A	C			PRT;	906 AA.
X	X		xxxxxx		
X	X				
X	X				
D	e		Sequence 2, Application US/08486270		
X	X				
C	C		Sequence 2, Application US/08486270		
C	C		Patent No. 5807689		
C	C		GENERAL INFORMATION:		
C	C		APPLICANT: Daggett, Lorrie		
C	C		APPLICANT: Ellis, Steven B.		
C	C		APPLICANT: Liaw, Chen		
C	C		APPLICANT: Pontsler, Aaron		
C	C		APPLICANT: Johnson, Edwin C.		
C	C		APPLICANT: Hess, Stephen D.		
C	C		TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,		
C	C		TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF		
C	C		NUMBER OF SEQUENCES: 13		
C	C		CORRESPONDENCE ADDRESS:		
C	C		ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark		
C	C		STREET: 444 South Flower Street, Suite 2000		
C	C		CITY: Los Angeles		
C	C		STATE: CA		
C	C		COUNTRY: USA		
C	C		ZIP: 90071		
C	C		COMPUTER READABLE FORM:		
C	C		MEDIUM TYPE: Floppy disk		
C	C		COMPUTER: IBM PC compatible		
C	C		OPERATING SYSTEM: PC-DOS/MS-DOS		
C	C		SOFTWARE: Patentin Release #1.0, Version #1.25		
C	C		CURRENT APPLICATION DATA:		
C	C		APPLICATION NUMBER: US/08/486,270		
C	C		FILING DATE: 02-JUN-1994		
C	C		CLASSIFICATION: 435		
C	C		PRIOR APPLICATION DATA:		
C	C		APPLICATION NUMBER: US 08/072,574		
C	C		FILING DATE: 04-JUN-1993		
C	C		ATTORNEY/AGENT INFORMATION:		
C	C		NAME: Reiter, Stephen E.		
C	C		REGISTRATION NUMBER: 31,192		
C	C		REFERENCE/DOCKET NUMBER: FP41 9772		
C	C		TELECOMMUNICATION INFORMATION:		
C	C		TELEPHONE: 619-546-4737		
C	C		TELEFAX: 619-546-9392		
C	C		INFORMATION FOR SEO ID NO: 2:		
C	C		SEQUENCE CHARACTERISTICS:		
C	C		LENGTH: 906 amino acids		
C	C		TYPE: amino acid		
C	C		TOPOLOGY: linear		
C	C		MOLECULE TYPE: protein		
S	Q		SEQUENCE 906 AA; 101292 MW; 4407237 CN;		
Q	U		Query Match	2.7%; Score 186; DB 1; Length 906;	
			Best Local Similarity 36.1% Pred. No. 3,11e-04;		
			Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0;		
D	B		159 VIGPESSVAIOVNOLDFPIDPIATASITSDSKTLYTFELRYVPSDTLQARAHLDI	218	
		: : : : : : : : : : : : : : : : : :			
O	y		130 YFGGPCPSTSIASISLGWNLVOLSFATPPVLADKKKPYFFPRTPVDNAVPAILKL	189	
		:	: : : : : : : : : : : :		
D	B		219 VKRNMVTYSAY	230	
		: : : :			
O	y		190 LKHQMKRVGTL	201	

RESULT 12
ID US-08-367-264-2 STANDARD; PRT: 906 AA.
XX
AC xxxxxx
XX
XX
DE Sequence 2, Application US/08367264
XX
CC Sequence 2, Application US/08367264
CC Patent No. 6001581
CC GENERAL INFORMATION:
CC APPLICANT: Daggett, Lorrie
CC APPLICANT: Ellis, Steven B.
CC APPLICANT: Liaw, Chen
CC APPLICANT: Pontsler, Aaron
CC APPLICANT: Johnson, Edwin C.
CC APPLICANT: Hess, Stephen D.
CC TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
CC TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
CC STREET: 444 South Flower Street, Suite 2000
CC CITY: Los Angeles
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/367,264
CC FILING DATE: 02-JUN-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/072,574
CC FILING DATE: 04-JUN-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Reiter, Stephen E.
CC REGISTRATION NUMBER: 31,192
CC REFERENCE/DOCKET NUMBER: FP41 9772
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-546-4737
CC TELEFAX: 619-546-9392
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 906 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 906 AA; 101292 MW; 4407237 CN;
SQ
Query Match 2.7%; Score 186; DB 3; Length 906;
Best Local Similarity 36.1%; Pred. No. 3.11e-04;
Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0;
Db 159 VIGPGSSVAIQVNLQJLFDIPQIAYSATSIDLSDKTYKFLRVVPSDPTLQARMLDI 218
OY 130 VFGVCPSTSTIAESLOGMNLVQLSFAATTPVLADKKKPYFFKRVPSDNAVNPAILKL 189
Db 219 VKRYNMTYVSAY 230
OY 190 LKHQMKRVGTL 201
RESULT 13
ID US-08-687-289A-7 STANDARD; PRT: 1056 AA.
XX
AC xxxxxx

XX
DT
XX
DE Sequence 7, Application US/08687289A
XX
CC Sequence 7, Application US/08687289A
CC Patent No. 5981195
CC GENERAL INFORMATION:
CC APPLICANT: Fuller, Forrest H.
CC APPLICANT: Krapcho, Karen J.
CC APPLICANT: Hamerland, Lance G.
CC TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
CC TITLE OF INVENTION: IDENTIFYING COMPOUNDS ACTIVE AT
CC TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTORS AND
CC TITLE OF INVENTION: THE USE OF SUCH COMPOUNDS IN THE
CC TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: 633 West Fifth Street
CC CITY: Suite 4700
CC STATE: California
CC COUNTRY: U.S.A.
CC ZIP: 90071-2066
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB
CC MEDIUM TYPE: storage
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: IBM P.C. DOS 5.0
CC SOFTWARE: Fastseq for Windows 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/687,289A
CC FILING DATE: July 25, 1996
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 60/001,526
CC FILING DATE: July 26, 1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Warburg, Richard J.
CC REGISTRATION NUMBER: 32,327
CC REFERENCE/DOCKET NUMBER: 220/004
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1056 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC SEQUENCE 1056 AA; 117663 MW; 5988966 CN;
SQ
Query Match 2.7%; Score 186; DB 2; Length 1056;
Best Local Similarity 36.1%; Pred. No. 3.11e-04;
Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0;
Db 159 VIGPGSSVAIQVNLQJLFDIPQIAYSATSIDLSDKTYKFLRVVPSDPTLQARMLDI 218
OY 130 VFGVCPSTSTIAESLOGMNLVQLSFAATTPVLADKKKPYFFKRVPSDNAVNPAILKL 189
Db 219 VKRYNMTYVSAY 230
OY 190 LKHQMKRVGTL 201
RESULT 14
ID US-08-687-289A-8 STANDARD; PRT: 1056 AA.
XX
AC xxxxxx

XX
DE
XX
XX
Sequence 8, Application US/08687289A
CC
XX
Sequence 8, Application US/08687289A
CC
Patent No. 5981195
CC
GENERAL INFORMATION:
CC
APPLICANT: Fuller, Forrest H.
CC
APPLICANT: Krapcho, Karen J.
CC
APPLICANT: Hammerland, Lance G.
CC
TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
CC
TITLE OF INVENTION: IDENTIFYING COMPOUNDS ACTIVE AT
CC
TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTORS AND
CC
TITLE OF INVENTION: THE USE OF SUCH COMPOUNDS IN THE
CC
TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS
CC
NUMBER OF SEQUENCES: 8
CC
CORRESPONDENCE ADDRESSES:
CC
ADDRESSEE: Lyon & Lyon
CC
STREET: 633 West Fifth Street
CC
STREET: Suite 4700
CC
CITY: Los Angeles
CC
STATE: California
CC
COUNTRY: U.S.A.
CC
ZIP: 90071-2066
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC
MEDIUM TYPE: storage
CC
COMPUTER: IBM Compatible
CC
OPERATING SYSTEM: IBM P.C. DOS 5.0
CC
SOFTWARE: FastSeq for Windows 2.0
CC
CURRENT APPLICATION DATA:
CC
APPLICATION NUMBER: US/08/687,289A
CC
FILING DATE: July 25, 1996
CC
CLASSIFICATION: 435
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: 60/001,526
CC
FILING DATE: July 26, 1995
CC
ATTORNEY/AGENT INFORMATION:
CC
NAME: Warburg, Richard J.
CC
REGISTRATION NUMBER: 32,327
CC
REFERENCE/DOCKET NUMBER: 220/004
CC
TELECOMMUNICATION INFORMATION:
CC
TELEPHONE: (213) 489-1600
CC
TELEFAX: (213) 955-0440
CC
TELEX: 67-3510
CC
INFORMATION FOR SEQ ID NO: 8:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 1056 amino acids
CC
TYPE: amino acid
CC
STRANDEDNESS: single
CC
TOPOLOGY: linear
CC
MOLECULE TYPE: Protein
CC
SEQUENCE 1056 AA; 117600 MW; 5991921 CN;
SQ
Query Match 2.7%; Score 186; DB 2; Length 1056;
Best Local Similarity 36.1%; Pred. No. 3.11e-04;
Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0;
Db 159 VIGPSSVAIQVONLLDFDIPQIAYSATSIDSKTLKYKFLRVPSDILQARAMD I 218
QY 130 VFGGVCPSVTSIIASISLQGNVLVLSFAITPVLAADKKRYPFFRTVPSDNANVPAILKL 189
Db 219 VKRYNMTYVSAY 230
QY 190 LKHYYQMKRYGTL 201
RESULT 15
ID US-08-687-289A-5 STANDARD; PRT; 1058 AA.
XX
NC xxxxxx

XX
DE
XX
XX
Sequence 5, Application US/08687289A
CC
XX
Sequence 5, Application US/08687289A
CC
Patent No. 5981195
CC
GENERAL INFORMATION:
CC
APPLICANT: Fuller, Forrest H.
CC
APPLICANT: Krapcho, Karen J.
CC
APPLICANT: Hammerland, Lance G.
CC
TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
CC
TITLE OF INVENTION: IDENTIFYING COMPOUNDS ACTIVE AT
CC
TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTORS AND
CC
TITLE OF INVENTION: THE USE OF SUCH COMPOUNDS IN THE
CC
TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS
CC
NUMBER OF SEQUENCES: 8
CC
CORRESPONDENCE ADDRESSES:
CC
ADDRESSEE: Lyon & Lyon
CC
STREET: 633 West Fifth Street
CC
STREET: Suite 4700
CC
CITY: Los Angeles
CC
STATE: California
CC
COUNTRY: U.S.A.
CC
ZIP: 90071-2066
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CC
MEDIUM TYPE: storage
CC
COMPUTER: IBM Compatible
CC
OPERATING SYSTEM: IBM P.C. DOS 5.0
CC
SOFTWARE: FastSeq for Windows 2.0
CC
CURRENT APPLICATION DATA:
CC
APPLICATION NUMBER: US/08/687,289A
CC
FILING DATE: July 25, 1996
CC
CLASSIFICATION: 435
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: 60/001,526
CC
FILING DATE: July 26, 1995
CC
ATTORNEY/AGENT INFORMATION:
CC
NAME: Warburg, Richard J.
CC
REGISTRATION NUMBER: 32,327
CC
REFERENCE/DOCKET NUMBER: 220/004
CC
TELECOMMUNICATION INFORMATION:
CC
TELEPHONE: (213) 489-1600
CC
TELEFAX: (213) 955-0440
CC
TELEX: 67-3510
CC
INFORMATION FOR SEQ ID NO: 5:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 1058 amino acids
CC
TYPE: amino acid
CC
STRANDEDNESS: single
CC
TOPOLOGY: linear
CC
MOLECULE TYPE: Protein
CC
SEQUENCE 1058 AA; 118709 MW; 5901398 CN;
SQ
Query Match 2.7%; Score 186; DB 2; Length 1058;
Best Local Similarity 36.1%; Pred. No. 3.11e-04;
Matches 26; Conservative 21; Mismatches 25; Indels 0; Gaps 0;
Db 159 VIGPSSVAIQVONLLDFDIPQIAYSATSIDSKTLKYKFLRVPSDILQARAMD I 218
QY 130 VFGGVCPSVTSIIASISLQGNVLVLSFAITPVLAADKKRYPFFRTVPSDNANVPAILKL 189
Db 219 VKRYNMTYVSAY 230
QY 190 LKHYYQMKRYGTL 201
Search completed: Wed Apr 19 22:07:42 2000
Job time : 24 secs.

QY 162 VLADKKKKYPPFRTPVPSDNANVPAILKLKLKHQMKRVGTLTLDQVRFSEVKNDLTGVLG 221
 Db 216 AGIEITTFQSFSPDPANVVKMLKRODARIYGLTFETEARVFEVYKRELFGKKYWEI 275
 QY 222 EDIEISDTSEFSNDPCTSVKRLKGNVDNRIILGFDONMAAKVFCACAEENNYGSKYOMII 281
 Db 276 IGVYADNMNF-KTY-DP-SINCTVDEMTAEVGHITTEIYMLNPANTRSISIMTQSOEVEK 332
 QY 282 PGMETPSMEVOYHTEANSSRCLRNLAAMEGYIGVDFEPLSSKOIKTISKTQOY-ER 340
 Db 333 LTRKLKRPDEETGFOEAPLAYDAIMALALANKTSGG--GGRSGVRLDEPNYNNQITTD 390
 QY 341 EYNN-KRSGVPSKPH-G-YAIDGIWIAKTQORAMETLHAASSRHORIDEPNYTDHTLGR 397
 Db 391 QIYRAMNSSFEVSGHYVFPDASSGRMAWTILIEOLGSGYKIKIGYDSTKDDL-SKT 449
 QY 398 IILNMMNTEFEGYGVYVF-RNGERMGTIKFTQFOSREKVEYNAVAATLEIINDTI 456
 Db 450 KWIGSPADDTLVTKTRFSLQKLEISVSLSGIYLAIVVCLSPFNYNSHVRYIONSQ 509
 QY 457 RFQSEPPKDKTIIIEQLRKISLPLYSILSLTILIGMAMAFLEFNKRNOKLIKMS 516
 Db 510 PNLNMLTAVGCSLAAVFPGLDGYHIGNQPFVPCQARLMLLGLGSLGYSMTKIM 569
 QY 517 PYMNLILIGMLSYASIFLGLDGSFVSEKTFELCTVRTWILTVGYTAFGAMFAKTW 576
 Db 570 WYHYVFTKKEKKERKTLERKLYATYGLLVGMVDLTALWQYVDPILHRIETFAKEP 629
 QY 577 RVHAIF--KNVKKM-KKIIIDOKLIVYIGMLLIDLCILCQWADVPLRTRVERKYSMPD 633
 Db 630 KEDIVSILIPOLEHSCSRKMTWLGIFYGYKGLLLGLIFLAYETKSVSTEKINDHRAV 689
 QY 634 PAGRISTIRPLEHCEHNTHTMILGIVAYKGLMLFECFLAMETRNVSIPALDSKTYG 693
 Db 690 MAIYNVAVCLITAPVTMLSSQDAPAFASLAIVSSYITLVLFVPMKRLITRGE 748
 QY 694 MSYVNVGIMCITGAIVSFLTRDQPNVQFCIVALYIFCSTITLCIVFVPKLITLRTND 752
 RESULT 2
 ID W40118 standard; Protein; 844 AA.
 AC W40118;
 DT 03-JUN-1998 (first entry)
 DE Rat GABA-BR1b receptor protein.
 KW Gamma-aminobutyric acid; GABA-BR1b receptor; rat; brain; agonist;
 KW Inhibitory neurotransmitter; peripheral nervous system; antagonist;
 KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
 KW epilepsy; cognitive function.
 OS Rattus norvegicus.
 PN MO9746675-A1.
 PD 11-DEC-1997;
 PF 19-MAR-1997; E01370.
 PR 22-NOV-1996; US-756091.
 PR 30-MAY-1996; US-655716.
 PA (NOVS) NOVARTIS AG.
 PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
 DR WPI: 98-042183/04.
 DR N-PSDB: V10266.
 PT Purified GABA-B receptor or receptor protein - and antagonists of
 PT these which may be useful in treating nervous system disorders
 CC Claim 4; Page 74-79; 108pp; English.
 CC This sequence represents a novel rat GABA-B receptor protein.
 CC GABA-BR1b (gamma-aminobutyric acid) is the major inhibitory
 CC neurotransmitter found in the brain and peripheral nervous system
 CC and this receptor may be used for the identification of GABA-B
 CC receptor agonists and antagonists. Such proteins may be used in
 CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
 CC bronchial inflammation or asthma or to improve cognitive function.
 CC GABA-B receptor ligands and probes derived from this sequence can be
 CC used to assay for GABA-B receptors or DNA encoding them.
 SQ Sequence 844 AA;

Query Match

24.5%; Score 1690; DB 1; Length 844;

Best Local Similarity 35.4%; Pred. No. 1,18e-124;
 Matches 268; Conservative 194; Mismatches 271; Indels 23; Gaps 21;

Db 2 GREGCPPTVGMPLPLILVMAAGVAPYMAASHPLRPHRVPVPHSSERRAVITCAL-PP 60
 QY 11 PPPPPPPPPARILLILLPL--LLPL-APGAWGMAGPR-PP-PSSPLSI-MGIMPLT 65
 Db 61 MSGWPG-GOACQPAYEMALDEVNSRDLIPDEYELKIHHDSCDPGQATKYLEYLND 119
 QY 66 KEVAKSGISGRVLPVAVELIETIRNE-SLRPEFLDLRLYTECDNAGKAFYAIKYG 124
 Db 120 PIKIIIMP-CSSSTVLAEAARMNLIVLSYSSSPALSNROREPTFRTHPSATLNP 178
 QY 125 PNLAVFVGCVPSVTIILAESLOGMNLVOLSPAATTPLYADKKKYPPFRTPVSDNANVP 184
 Db 179 TRVKELEKMGKKIATIOOTTEVFTSTLDDLEERKEAGIEITTFQSFSDPNAVVKIK 238
 QY 185 AILKLKHQMKRVGTLTDVORFSEVNRDLTGVLGEDIESTDESEFSNDPCTSVKLIK 244
 Db 239 RODARIIVGLFETEARKVFCEYKRELFGKKYVWFLGMVADNMNF-KTY-DP-SINCTV 295
 QY 245 GNDVRIILGFDONMAAKVFCACAEENNYGSKYOMIIPGMETPSMEVOYHTEANSSRCLR 304
 Db 296 EEMTEAVEGHITTEIYMLNPANTRSISIMTQSOEVEKTLKRLKRPDEETGFOEAPLAYD 355
 QY 305 KNLLAMEGYIGVDFEPLSSKOIKTISKTPOY-EREYNN-KRSGVPSKPH-G-YAID 360
 Db 356 AIALALANKTSGG--GGRSGVRLDEPNYNNQITDQIYRAMNSSFEVSGHYVFPDAS 413
 QY 361 GIWIAKTQORAMETLHAASSRHORIDEPNYTDHTLGRILNMMNTEFEGYGVYVF-RN 419
 Db 414 GSRMAWTILIEOLGSGYKIKIGYDSTKDDL-SKTDMKIGSPADDTLVTKTRFSLQ 472
 QY 420 GERMGTIKFTQFOSREKVEYNAVAATLEIINDIRROGSEPPKDKTIIIEQLRKISL 479
 Db 473 KLEISVSLSGIYLAIVVCLSPFNYNSHVRYIONSQPNLNLTAIVGCSLAAVFPGL 532
 QY 480 PLYSILSLTILIGMAMAFLEFNKRNOKLIKMSPYMNLILIGMLSYASIFLGL 539
 Db 533 DGYHIGRSOPFPVPCQARLMLLGLGSLGYSMTKIMWYHYVFTKKEKKERKTLERPK 592
 QY 540 DGSFVSEKTFELCTVRTWILTVGYTAFGAMFAKTWRVHAIF--KNVKKM-KKIIIDOK 596
 Db 593 LVAIVGLLVGMVDLTALWQYVDPILHRIETFAKEPKEDIVSILIPOLEHSCSRKMTW 652
 QY 597 LVIYVGMMLIDLCILCQWADVPLRTRVERKYMEDPAGROISIRPLEHCEHNTHTM 656
 Db 653 LGIFYGYKGLLLGLIFLAYETKSVSTEKINDHRAVGMAIYNVAVCLITAPVTMLSSQ 712
 QY 657 LGIYVAYKGLMLFECFLAMETRNVSIPALDSKTYGMSYVNVGIMCITGAIVSFLTRDQ 716
 Db 713 QDAAFASLAIVSSYITLVLFVPMKRLITRGE 748
 QY 717 PNVOFCIVALYIFCSTITLCIVFVPKLITLRTND 752
 RESULT 3
 ID W40117 standard; Protein; 793 AA.
 AC W40117;
 DT 03-JUN-1998 (first entry)
 DE Human GABA-BR1a/b receptor protein.
 KW Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
 KW Inhibitory neurotransmitter; peripheral nervous system; antagonist;
 KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
 KW epilepsy; cognitive function.
 OS Homo sapiens.
 PN WO9746675-A1.
 PD 11-DEC-1997;
 PF 19-MAR-1997; E01370.
 PR 22-NOV-1996; US-756091.
 PR 30-MAY-1996; US-655716.
 PA (NOVS) NOVARTIS AG.
 PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;

DR WPI: 98-042183/04.
DR N-PSDB: V10265.
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
PS Claim 4; Page 62-67; 108pp; English.
CC This sequence represents a novel human GABA-B receptor protein,
CC GABA-BR1A/D. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them.
SQ Sequence 793 AA;

Query Match 24.4%; Score 1687; DB 1; Length 793;
Best Local Similarity 36.2%; Pred. No. 2,08e-124;
Matches 249; Conservative 180; Mismatches 243; Indels 16; Gaps 14;

Db 17 GQACOPAVEMALEEDVNSRRDILPDYELKLHHSKCDPGQATKYLYELLNDPIKILMP 76
QY 74 GRGVPAVELAIQIQRNE-SLRPFYDLRLDYEDCNAGKAKFYDAIKYGNHLMWFG 132
Db 77 G-CSSVSTLVAEARMNLIYLSGSSSPALSNORPPTFFRTHSATLHNPYKLEFK 135
QY 133 GVCPSVTSIIASLQGMNLVOLSFATTPYVLADKKKYFFFTYPSDNAVNALIKLKH 192
Db 136 WGMKRIATIQOTTEVTSTLDLEERVKAGIEITFRSFPSPDAVPVKNLRDARIIV 195
QY 193 YOMKRVGTLTDVQRFSEVRNDLTGVLGEDIEISDTSFSDPCTSVKRLKGNVRIIL 252
Db 196 GLPYTEARKEVCEYKKEFLFGKYYWFLIGWYADNMF-KTY-DP-SINCTVEEMTEAVE 252
QY 253 GQFDONMAAKVFCACAEENMYGSKYQWIIIPGMYEBSMWEQVHTBANSRCLRNILAME 312
Db 253 GHITTEIYMLNPANTRISNMTSOEFVEKLRKLKRHEEFGQEPAPLAYDAIMALALA 312
QY 313 GYGVDFEFLSKQIKTIGSKTPQY-EREYNN-KRSVGSPSKFH-G-YAYDGIWVIAT 368
Db 313 LNKTSGG--GGRSGVRLDEPNYNNOTITDQIYRAMNSSFEVSGHVYFDASGRMAWTL 370
QY 369 LQRAMETTLHASSRHRIODFNYTDHILGRILNMANNEFTFGVGYQVY-RNGERMGTIK 427
Db 371 IEOLGSGYKKIKGYDSTKDLSSW-SKTDKWIIGSPPAQDTVIKTFRLSQKLFISV 429
QY 428 FTQFQDSREVKYGEYNAVDLTLEIINDTIRFQGSSEPPKDTIILEQLRKISLPLYSILSA 487
Db 430 LSSIGIYLAIVCLSFENIYNSHRYIYONSOPNLNLTAAGCSLAAPFLGIDGYHIGRN 489
QY 488 LITLIGIMASAFLEFNIRNOKLIKMSSPYNNLLILGMLSTYASIFLFGIDGSFVSEK 547
Db 490 QPPEVCQARMLMLGIFSLGYSGMTKIMWHTVFTKKEEKEKEMRKTLLEPKLYATVGL 549
QY 548 TFEITLCIVRTWILTYGTAFGAMFAKTRVHAIF--KNVKKM-KKIIKQKLLVIYVGM 604
Db 550 VGMDEVTLTAIMQVDPILRTIETFAKEEPKEDIVSILPOLHSCSRKKNNTWLGIFYGK 609
QY 605 LTLIDLCILICQMAVDPLRRTVEKYSMEPPDAGDISIRPLEHCENTHMTWILGIYAYK 664
Db 610 GLTLLIGFLAVETKSTYSTEKINDHRAVGMAYNAVLCILITAPVTMILSSOODAFAFA 669
QY 665 GILMLFGCLAMETRNVSIPALNDSKICYGMSYVNGIMCIIIGAAVSFLTRDQPNVOFCIV 724
Db 670 STAIYVSSITTLVLFVPMKRLITRGE 697
QY 725 ALVIIFCSITTLCLVFPKILITLTPND 752

RESULT 4
ID W40116 standard; Protein; 960 AA.
AC W40116;
DT 03-JUN-1998 (first entry)

DE Rat GABA-BR1a receptor protein.
KW Gamma-aminobutyric acid; GABA-BR1a receptor; rat; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
OS Rattus norvegicus.
PN M09746675-A1.
PD 11-DEC-1997.
PE 19-MAR-1997; E01370
PR 22-NOV-1996; US-756091.
PR 30-MAY-1996; US-655716.
PI Bettler B, Bitliger H, Froestl W, Kaupmann K, Michel SJ.
DR WPI: 98-042183/04.
DR N-PSDB: V10264.
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
PS Claim 4; Page 50-56; 108pp; English.
CC This sequence represents a novel rat GABA-B receptor protein,
CC GABA-BR1a. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them.
SQ Sequence 960 AA;

Query Match 24.4%; Score 1682; DB 1; Length 960;
Best Local Similarity 36.2%; Pred. No. 5,39e-124;
Matches 249; Conservative 178; Mismatches 245; Indels 16; Gaps 14;

Db 184 GQACOPAVEMALEEDVNSRRDILPDYELKLHHSKCDPGQATKYLYELLNDPIKILMP 243
QY 74 GRGVPAVELAIQIQRNE-SLRPFYDLRLDYEDCNAGKAKFYDAIKYGNHLMWFG 132
Db 244 G-CSSVSTLVAEARMNLIYLSGSSSPALSNORPPTFFRTHSATLHNPYKLEFK 302
QY 133 GVCPSVTSIIASLQGMNLVOLSFATTPYVLADKKKYFFFTYPSDNAVNALIKLKH 192
Db 303 WGMKRIATIQOTTEVTSTLDLEERVKAGIEITFRSFPSPDAVPVKNLRDARIIV 362
QY 193 YOMKRVGTLTDVQRFSEVRNDLTGVLGEDIEISDTSFSDPCTSVKRLKGNVRIIL 252
Db 363 GLPYTEARKEVCEYKKEFLFGKYYWFLIGWYADNMF-KTY-DP-SINCTVEEMTEAVE 419
QY 253 GQFDONMAAKVFCACAEENMYGSKYQWIIIPGMYEBSMWEQVHTBANSRCLRNILAME 312
Db 420 GHITTEIYMLNPANTRISNMTSOEFVEKLRKLKRHEEFGQEPAPLAYDAIMALALA 479
QY 428 FTQFQDSREVKYGEYNAVDLTLEIINDTIRFQGSSEPPKDTIILEQLRKISLPLYSILSA 487
Db 480 LNKTSGG--GGRSGVRLDEPNYNNOTITDQIYRAMNSSFEVSGHVYFDASGRMAWTL 537
QY 369 LQRAMETTLHASSRHRIODFNYTDHILGRILNMANNEFTFGVGYQVY-RNGERMGTIK 427
Db 538 IEOLGSGYKKIKGYDSTKDLSSW-SKTDKWIIGSPPAQDTVIKTFRLSQKLFISV 596
QY 428 TFEITLCIVRTWILTYGTAFGAMFAKTRVHAIF--KNVKKM-KKIIKQKLLVIYVGM 604
Db 597 LSSIGIYLAIVCLSFENIYNSHRYIYONSOPNLNLTAAGCSLAAPFLGIDGYHIGRS 656
QY 488 LITLIGIMASAFLEFNIRNOKLIKMSPPYNNLLILGMLSTYASIFLFGIDGSFVSEK 547
Db 657 QPPEVCQARMLMLGIFSLGYSGMTKIMWHTVFTKKEEKEKEMRKTLLEPKLYATVGL 716
QY 548 TFEITLCIVRTWILTYGTAFGAMFAKTRVHAIF--KNVKKM-KKIIKQKLLVIYVGM 604
Db 717 VGMDEVTLTAIMQVDPILRTIETFAKEEPKEDIVSILPOLHSCSRKKNNTWLGIFYGK 776
QY 605 LTLIDLCILICQMAVDPLRRTVEKYSMEPPDAGDISIRPLEHCENTHMTWILGIYAYK 664

CC glutamatergic ligands. Its amino acid sequence was determined from
 CC cDNA clones (see also T38322) obt'd. from a human retinal cDNA library.
 CC A splice variant has an alternative N-terminal sequence (see also
 CC W01100). Recombinant receptors, practically free of contamination
 CC by other receptors, can be produced in host cells. The receptors,
 CC and cells expressing them, are used in drug screening to identify
 CC cpts. that modulate mGluR6.
 SQ Sequence 877 AA;

Query Match 3.3%; Score 225; DB 1; Length 877;
 Best Local Similarity 21.5%; Pred. No. 8.74e-07;
 Matches 60; Conservative 91; Mismatches 106; Indels 22; Gaps 19;

Db 592 LAVGIATFTVVAFTFVRNPPPIVIRASGRELSTVLLTGIFLYIA-I-TF-L--MVAEP 645
 Qy 488 LTIIGMTASAFLEFNINRNOIKIKSSPPMNNLIIIGMLSYASIFLGLDGSFVSEK 547
 Db 646 G-AAVCAARLELGLGTTLSALLTKTRNRYRFEQGRKSVTPPPISPTSQLVTFSL 704
 Qy 548 TFEFLCTVRWILTVGYTTAFGAMFAKTRVHAIFKNVK--MKKK-IIRKOKLIVYGGM 604
 Db 705 TSLGVGMIMLGRPPHSVID-YE-EQRTVDEQA-RGVLR-CDMSDLSL-IGCL-GY- 757
 Qy 605 LLIIDLCTILICQAVDPLRRTVEKSMEDPPAGRDISIRPLEHCENTHMTWIGIYAYK 664
 Db 758 SLILMWTCTVYAIKRGVPEFNEAKPIGFTMTTCIIMLAFVPIFGTAQSAEKIYIQ 816
 Qy 665 GLMLFEGCFIAMETRNVSIP-ALNDSKYIGMSYVNGVICIGAAVSFLTRDQPNVQFC- 722
 Db 817 TTTITVLSLSASVSLGMLYVPKTYVILFHPDONVQRK 855
 Qy 723 IVALVI-I-FCSTITLCTVFPKLTITLRNPDAVONRR 759

RESULT 8
 ID W49928 standard; protein; 908 AA.
 AC W49928;
 DT 09-JUN-1998 (first entry)
 DE Human metabotropic glutamate receptor (mGluR).
 KW Metabotropic glutamate receptor; mGluR; screening; stroke; epilepsy;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease.
 OS Homo sapiens.
 PN W09748724-A2.
 PD 24-DEC-1997.
 PE 20-FEB-1997; U09025.
 PR 21-FEB-1996; US-604298.
 PA (NPSP-) NPS PHARM INC.
 PI Fuller FH, Hammerland LG, Slimin RT, Stormann TM;
 DR WPI; 98-063076/06.
 DR N-PSDB; V17116.
 PT Novel human metabotropic glutamate receptor - for screening
 PT compounds useful for treating e.g. stroke, epilepsy or diseases such
 PT as Alzheimer's, Parkinson's or Huntington's diseases
 PS Claim 7, Fig 1; 98pp; English.
 CC This is a novel human metabotropic glutamate receptor (mGluR). A
 CC purified or isolated nucleic acid of at least 15 nucleotides in length
 CC encoding at least 6 contiguous amino acids of the unique portion of this
 CC mGluR can be used to generate transgenic mammals by insertion of the
 CC nucleic acid into the mammalian genome. The mGluR can be used to screen
 CC for compounds which modulate its activity, especially in the
 CC physiological functions of convulsions, neuroprotection, neuronal death
 CC and development, central control of cardiac activity, waking, control of
 CC movement and control of vestibulo-ocular reflex. Such compounds can be used
 CC to treat glutamate excitotoxicity, global and focal ischemic and
 CC haemorrhagic stroke, head trauma, spinal cord injury, hypoxia-induced
 CC nerve damage, epilepsy or neurodegenerative diseases such as Alzheimer's,
 CC Parkinson's or Huntington's diseases.
 SQ Sequence 908 AA;

Query Match 3.3%; Score 231; DB 1; Length 908;
 Best Local Similarity 21.9%; Pred. No. 3.24e-07;
 Matches 62; Conservative 97; Mismatches 100; Indels 24; Gaps 21;

Db 590 VALLGII-ATFEVIVTFVRNPPPIVIRASGRELSTVLLTGIFLCYSITFLM-I-AA--PD 644
 Qy 488 LTIIGMTASAFLEFNINRNOIKIKSSPPMNNLIIIGMLSYASIFLGLDGSFVSEK 546
 Db 645 -TI-ICSEFRVFLGCMCSYAAALLTKTRIRIRIFEQGRKSTAKRFTSPASQVITTS 701
 Qy 547 KTFETLCTVTRWILTVGYTTAFGAMFAKTRVHAIFKNVK-K-KIIRKOKLIVYGG 603
 Db 702 LISVOLGVFVFWVDPPIIID-YG-EQRTLPDEKA-RGVLR-CDISDLSL-IGSL-GY 755
 Qy 604 MLIIIDLCTILICQAVDPLRRTVEKSMEDPPAGRDISIRPLEHCENTHMTWIGIYAY 663
 Db 756 SLILM-VTCTVYAIKRGVPEFNEAKPIGFTMTTCIIMLAFVPIFGTAQSAEKMTY 813
 Qy 664 KGLIMFEGCFIAMETRNVSIP-ALNDSKYIGMSYVNGVICIGAAVSFLTRDQPNVQFC 722
 Db 814 QTTITVLSLSASVSLGMLYVPKTYVILFHPDONVQRKRS 856
 Qy 723 -IVALVI-I-FCSTITLCTVFPKLTITLRNPDAVONRRQF 762

RESULT 9
 ID R82658 standard; protein; 912 AA.
 AC R82658;
 DT 20-DEC-1995 (first entry)
 DE Human mGluR4.
 KW Metabotropic glutamate receptor 4; mGluR4; stroke; epilepsy;
 KW Alzheimer disease; detection; diagnosis; therapy.
 OS Homo sapiens.
 FH Key
 FT domain
 FT 588..610
 FT /label= TMD-I
 FT /note= "transmembrane domain I"
 FT 625..645
 FT /label= TMD-II
 FT /note= "transmembrane domain II"
 FT 657..675
 FT /label= TMD-III
 FT /note= "transmembrane domain III"
 FT 699..720
 FT /label= TMD-IV
 FT /note= "transmembrane domain IV"
 FT 751..771
 FT /label= TMD-V
 FT /note= "transmembrane domain V"
 FT 786..807
 FT /label= TMD-VI
 FT /note= "transmembrane domain VI"
 FT 823..847
 FT /label= TMD-VII
 FT /note= "transmembrane domain VII"
 FT domain
 FT W09522609-A2.
 PN 24-AUG-1995.
 PE 21-FEB-1995; G00356.
 PR 21-FEB-1994; GB-003285.
 PR 01-AUG-1994; GB-015532.
 PA (WELL) WELLCOME FOUND LTD.
 PI Makoff AJ;
 DR WPI; 95-302715/39.
 DR N-PSDB; T03888.
 PT New isolated human metabotropic glutamate receptors - used for
 PT detection, diagnosis and therapy of diseases associated with the
 PT receptors, eg. stroke, epilepsy and Alzheimer's disease.
 PS Claim 2; Page 40-43; 55pp; English.
 CC mRNA from the human cerebellum was used to construct a cDNA
 CC library. cDNA was amplified by PCR primers (703896-97) based on rat
 CC mGluR4 sequences and with the primers given in T03898-99 to obtain
 CC cDNA encoding human mGluR4.
 SQ Sequence 912 AA;

Query Match 3.3%; Score 228; DB 1; Length 912;
 Best Local Similarity 21.6%; Pred. No. 5.32e-07;
 Matches 62; Conservative 98; Mismatches 100; Indels 27; Gaps 22;

Db 588 AVLPFLAVVG-IAATLEVVITFVRNDPTIVKASGRELSTVLLAGIFLCYATTEL--M- 643
 OY 483 SILSA-LTILGIMASAFLEFN-INKRNOKLIKSSPYMNNLITILGMLSTASIFLFGD 540
 Db 644 ---IAEPDLGT-CSLRRIEFLGMSISYALLTKTNRIYRIFEOGRSAPFISPASQ 699
 OY 541 GSPFVSEKTEFTLCTVRWLLTGTTAFGAMFAKTWRVHAIFKNVK--MKK-KIIOQKL 597
 Db 700 LAIFESLISLT-LGICWPFVVPSSHVV-DFOQRTLDPR-PA-RGVLK-CDISDLSL- 753
 OY 598 LVIYVGMILLIDLCILIC-WQAVDPLRTVEKYSMEPDPAQRODISIRPLEHCENTHMTIW 656
 Db 754 ICLL-GYSMLLV-TC-TVYAIKTRGVPEFNEAKPIGFTMYTTCIYWLAFIPFGTSQ 810
 OY 657 LGIYVAAKGLIMLFGCFLAMETRNVSIP-ALNDSKYIGMSVYVNGIMCIIGAASFLTRD 715
 Db 811 SADKLXIQTTLTVSVLSASVSLGMLYMPKYYIIIFHPQONVPRK 857
 OY 716 QPNVQFC-IVALVI-I-FCSTITLCLVFPVKLITLRTNPDATQNR 759

RESULT 10
 ID R72092 standard; Protein: 912 AA.
 AC R72092; 1995 (first entry)
 DT 26-SEP-1995
 DE Human mglur4.
 KW Human metabotropic glutamate receptor subtype 4; mglur4; hmglur4;
 KM signal transducer.
 OS Homo sapiens.
 PN WO9508627-A.
 PD 30-MAR-1995.
 PF 07-SEP-1994; E02991.
 PR 20-SEP-1993; EP-810663.
 PR 19-AUG-1994; GB-016553.
 PA (CIBA) CIBA GEIGY AG.
 PI Flor PJ, Kneopfel T, Kuhn R, Lindauer K, Puettnner I;
 DR WPI; 95-139596/18.
 DR N-PSDB; 089342.
 PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
 PT 7 - also corresp. DNA and antibodies, useful for identifying
 PT cpds. which modulate signal transduction activity
 PS Claim 2; Page 44-48; 110pp; English.
 CC Human metabotropic glutamate receptor subtype 4 (hmglur4) cDNA
 CC clones were isolated from a cerebellum cDNA library using a rat
 CC mglur4 probe. Clone cmr20 lacked the 5' end of the hmglur4 gene.
 CC PCR using human genomic or brain cDNA as template was used to
 CC obtain a complete gene sequence (given in 089342) encoding hmglur4
 CC (R72092). Recombinant hmglur4 was produced in mammalian cells.
 SO Sequence 912 AA;

Query Match 3.3%; Score 228; DB 1; Length 912;
 Best Local Similarity 21.6%; Pred. No. 5.32e-07;
 Matches 62; Conservative 98; Mismatches 100; Indels 27; Gaps 22;

Db 588 AVLPFLAVVG-IAATLEVVITFVRNDPTIVKASGRELSTVLLAGIFLCYATTEL--M- 643
 OY 483 SILSA-LTILGIMASAFLEFN-INKRNOKLIKSSPYMNNLITILGMLSTASIFLFGD 540
 Db 644 ---IAEPDLGT-CSLRRIEFLGMSISYALLTKTNRIYRIFEOGRSAPFISPASQ 699
 OY 541 GSPFVSEKTEFTLCTVRWLLTGTTAFGAMFAKTWRVHAIFKNVK--MKK-KIIOQKL 597
 Db 700 LAIFESLISLT-LGICWPFVVPSSHVV-DFOQRTLDPR-PA-RGVLK-CDMSDSL- 753
 OY 598 LVIYVGMILLIDLCILIC-WQAVDPLRTVEKYSMEPDPAQRODISIRPLEHCENTHMTIW 656
 Db 754 ICLL-GYSMLLV-TC-TVYAIKTRGVPEFNEAKPIGFTMYTTCIYWLAFIPFGTSQ 810
 OY 657 LGIYVAAKGLIMLFGCFLAMETRNVSIP-ALNDSKYIGMSVYVNGIMCIIGAASFLTRD 715
 Db 811 SADKLXIQTTLTVSVLSASVSLGMLYMPKYYIIIFHPQONVPRK 857

OY 716 QPNVQFC-IVALVI-I-FCSTITLCLVFPVKLITLRTNPDATQNR 759

RESULT 11
 ID R72095 standard; Protein: 481 AA.
 AC R72095;
 DT 26-SEP-1995 (first entry)
 DE Human mglur7 clone cmr5.
 KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
 KM signal transducer.
 OS Homo sapiens.
 PN WO9508627-A.
 PD 30-MAR-1995.
 PF 07-SEP-1994; E02991.
 PR 20-SEP-1993; EP-810663.
 PR 19-AUG-1994; GB-016553.
 PA (CIBA) CIBA GEIGY AG.
 PI Flor PJ, Kneopfel T, Kuhn R, Lindauer K, Puettnner I;
 DR WPI; 95-139596/18.
 DR N-PSDB; 089345.
 PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
 PT 7 - also corresp. DNA and antibodies, useful for identifying
 PT cpds. which modulate signal transduction activity
 PS Claim 8; Page 69-72; 110pp; English.
 CC Human metabotropic glutamate receptor subtype 7 (hmglur7) cDNA
 CC clones were isolated from cDNA libraries using a rat mglur4 probe.
 CC Fetal brain partial cDNA clone cmr5, encoding the protein given in
 CC R72095, was obtained. The missing 5' region of the clone was
 CC generated by PCR from brain cDNA. Sequence comparison of fetal
 CC brain and hippocampus clones indicated the existence of 2 subtypes
 CC of hmglur7 (R72097-98).
 SO Sequence 481 AA;

Query Match 3.1%; Score 214; DB 1; Length 481;
 Best Local Similarity 22.9%; Pred. No. 5.34e-06;
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

Db 172 LAMLGIT-ATIFVMAFFIRYNDPTIVKASGRELSTVLLAGIFLCY--ITF-L--MTA- 223
 OY 488 LTILGIMASAFLEFN-INKRNOKLIKSSPYMNNLITILGMLSTASIFLFGDSFVSE 546
 Db 224 KPDVAVCSRRVFLGIMCISYALLTKTNRIYRIFEOGRSAPFISPASQ 283
 OY 547 KTFEFTLCTVRWLLTGTTAFGAMFAKTWRVHAIFKNVK-K--KIIOQKLVIYIG 603
 Db 284 LISVOLLGFT-WGVDPNNIID-YD-EHKTMNPGA-RGVLK-CDITDQI-ICSL-G 336
 OY 604 MLTIDL-CILICWQAVDPLRTVEKYSMEPDPAQRODISIRPLEHCENTHMTIYIYA 662
 Db 337 YSILLV-TC-TVYAIKTRGVPEFNEAKPIGFTMYTTCIYWLAFIPFGTAQSAEKLY 394
 OY 663 YKGLIMLFGCFLAMETRNVSIPA-LNDSKYIGMSVYVNGIMCIIGAASFLTRDPNVQF 721
 Db 395 IOTTTLTISNLSASVALGMLYMPKYYIIIFHPELVQKRKSF 438
 OY 722 C-IVALVI-I-FCSTITLCLVFPVKLITLRTNPDATQNRROF 762

RESULT 12
 ID R72093 standard; Protein: 867 AA.
 AC R72093;
 DT 26-SEP-1995 (first entry)
 DE Human mglur7 clone cmr2.
 KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
 KM signal transducer.
 OS Homo sapiens.
 PN WO9508627-A.
 PD 30-MAR-1995.
 PF 07-SEP-1994; E02991.
 PR 20-SEP-1993; EP-810663.
 PR 19-AUG-1994; GB-016553.
 PA (CIBA) CIBA GEIGY AG.
 PI Flor PJ, Kneopfel T, Kuhn R, Lindauer K, Puettnner I;

Query Match	3.1%;	Score 214;	DB 1;	Length 867;
Best Local Similarity	22.9%;	Pred. No. 5.34e-06;		
Matches	65;	Conservative	87;	Mismatches 106;
			Indels	26;
			Gaps	22;

RESULT	13
ID	R72097 standard; Protein; 915 AA

Query Match	3.18;	Score 217;	DB 1;	Length 915
Best Local Similarity	22.98;	Pred. No. 3.27e-06;		

722 C-IVALVI-I-FCSTITLCLVFPKLTILRTNPDAQONRRQOF 7622

cc mediating inhibition of transmitter release at particular
cc glutamatergic synapses.
sq Sequence 915 AA;

Query Match	3.18;	Score 214;	DB 1;	Length 915;
Best Local Similarity	22.98;	Pred. No. 5.34e-06;		
Matches	65;	Conservative	87;	Mismatches 106; Indels 26; Gaps 22

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Db 597 LAMLGII-ATIFVMAFIRYNDPIYASGRELSYVLTGIFLCY--ITTF-L--MTA- 648
Qy 488 LTIIGMIMASAFLEFN-IKRNRKLIKASSPNNIILIGMLSTASIFLGLDGSFVSE 546
Db 649 KPDVAVCSFRFVFLGICMCISYVALLTKNRIYRIFEGQKSVTPARLISPTSLATSS 708
Qy 547 KTFETLCTVTRWILTVGYTAFGAFKTRVHAIFKNYKMK-K--KIIDQKLLVIYGG 603
Db 709 LISVOLLGVFI-WGVDPPIIID-YD-EHKTMNPEQA-RGVLK-CDITDLOI-ICSL-G 761
Qy 604 MLTIDL-CLICQAVDPLRTRVEKTSMEPDAGRDISIRPLEHCENTHMTIWLGIYVA 662
Db 762 YSILLAV-TC-TYVAIKTRGVNPNENAKPIGFTWYTCIWLAFIPIFGTAQSAEKLY 819
Qy 663 YKGLIMFGCFLEMETRNVSIPA-LNDSKYIGMSYVNGVICIGAAVSFLTRDQPNVOF 721
Db 820 IQTTTLISNMLASVALGMLYMPKYIIIFHELNQKRRSF 863
Qy 722 C-YVALVI-I-FCSTITLCLVFPVKLITLTNPDAATQNRROF 762

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RESULT 15

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ID R72098 standard; Protein; 922 AA.
AC R72098;
DE 26-SEP-1995 (first entry)
DE Human mglur7b.
KW Human metabotropic glutamate receptor subtype 4; mglur7; hmgLur7;
KW signal transducer.
OS Homo sapiens.
PN WC9508627-A.
PD 30-MAR-1995.
PE 07-SEP-1994; E02991.
PR 20-SEP-1993; EP-810663.
PR 19-AUG-1994; GB-016533.
PA (CIBA ) CIBA GEIGY AG.
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puetner I;
DR WPI; 95-139596/18.
DR N-PSDB; 089348.
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
PT 7 - also corresp. DNA and antibodies, useful for identifying
PT cpds. which modulate signal transduction activity
PS Claim 7; Page 95-99; 110pp; English.
CC Human metabotropic glutamate receptor subtype 7 (hmgLur7) cDNA
CC clones were isolated from fetal brain and hippocampus cDNA libraries
CC using a rat mglur4 probe, and the 5' region missing from these
CC clones was generated by PCR from brain cDNA. Sequence comparison of
CC fetal brain and hippocampus clones indicated the existence of 2
CC subtypes of hmgLur7, hmgLur7a (given in R72097) and hmgLur7b
CC (R72098). Full-length cDNA clones (Q89347-48) encoding these
CC proteins were expressed in mammalian cells.
SQ Sequence 922 AA;

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Query Match 3.1%; Score 214; DB 1; Length 922;

Best Local Similarity 22.9%; Pred. No. 5,34e-06;

Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

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Db 597 LAMLGII-ATIFVMAFIRYNDPIYASGRELSYVLTGIFLCY--ITTF-L--MTA- 648
Qy 488 LTIIGMIMASAFLEFN-IKRNRKLIKASSPNNIILIGMLSTASIFLGLDGSFVSE 546
Db 649 KPDVAVCSFRFVFLGICMCISYVALLTKNRIYRIFEGQKSVTPARLISPTSLATSS 708
Qy 547 KTFETLCTVTRWILTVGYTAFGAFKTRVHAIFKNYKMK-K--KIIDQKLLVIYGG 603
Db 709 LISVOLLGVFI-WGVDPPIIID-YD-EHKTMNPEQA-RGVLK-CDITDLOI-ICSL-G 761
Qy 604 MLTIDL-CLICQAVDPLRTRVEKTSMEPDAGRDISIRPLEHCENTHMTIWLGIYVA 662
Db 762 YSILLAV-TC-TYVAIKTRGVNPNENAKPIGFTWYTCIWLAFIPIFGTAQSAEKLY 819
Qy 663 YKGLIMFGCFLEMETRNVSIPA-LNDSKYIGMSYVNGVICIGAAVSFLTRDQPNVOF 721
Db 820 IQTTTLISNMLASVALGMLYMPKYIIIFHELNQKRRSF 863

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Qy 722 C-YVALVI-I-FCSTITLCLVFPVKLITLTNPDAATQNRROF 762

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